

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSR AR LNTEMGVVIE SPKIAEQM
 451 TLADTSPEYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AAKILS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60	
m987.pep	MKTRSLISI LCLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY						
a987	MKTRSLISI LCLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY	10	20	30	40	50	60
	70	80	90	100	110	120	
m987.pep	LLNDPHEAFAARAALIESAEHSLDI QYYIWRNDISGRLLFNLVLA AERGVVRVRLDDN						
a987	LLNDPHEAFAARAALIESAEHSLDI QYYIWRNDISGRLLFNLVLA AERGVVRVRLDDN	70	80	90	100	110	120
	130	140	150	160	170	180	
m987.pep	NTRGLDDLLL ALDSHPNIEVRLFNPVLRKW RALGYLTDFPRLNRRMHNKSF TADNRATI						
a987	NTRGLDDLLL ALDSHPNIEVRLFNPVLRKW RALGYLTDFPRLNRRMHNKSF TADNRATI	130	140	150	160	170	180
	190	200	210	220	230	240	
m987.pep	LGGRNIGDEYFKVGEDTVFADLDI LATGSVVGEVSHDFDRYWASHSAHNATRI IRSGDIG						
a987	LGGRNIGDEYFKVGEDTVFADLDI LATGSVVGEVSHDFDRYWASHSAHNATRI IRSGNIG	190	200	210	220	230	240
	250	260	270	280	290	300	
m987.pep	KGLQALGYN D ETSRHALLRYRETVEQSPLYQKIQTG C IDWQSVRTRL ISDDPAKGLDRDR						
a987	KGLQALGYN D ETSRHALLRYRETVEQSPLYQKIQTG C IDWQSVQTRL ISDDPAKGLDRDR	250	260	270	280	290	300
	310	320	330	340	350	360	
m987.pep	RKPPIAGR LQDALKQPEKSVYL VSPYFVPTKSGT DALAKLVQDGIDVTVL TNLSQATDVA						
a987	RKPPIAGR LQDALKQPEKSVYL VSPYFVPTKSGT DALAKLVQDGIDVTVL TNLSQATDVA	310	320	330	340	350	360
	370	380	390	400	410	420	
m987.pep	AVHSGYVKYR KPLLKAGIKLYE LQPNHAVP ATKD GLTGSSV TSLHAKTFIVDGKRIFIG						
a987	AVHSGYVKYR KPLLKAGIKLYE LQPNHAVP ATKD GLTGSSV TSLHAKTFIVDGKRIFIG	370	380	390	400	410	420
	430	440	450	460	470	480	
m987.pep	SFNLDPRSAR LNTEMGVVI ESKIAEQMERTLADTT PAYAYRVTL DRHNR LQWHD PATRK						
a987	SFNLDPRSAR LNTEMGVVI ESKIAEQMERTLADTSPEYAYRVTL DRHNR LQWHD PATRK	430	440	450	460	470	480
	490	500	509				
m987.pep	TYPNEPEAKLWKRIA AAKILSLLPIEGLLX						
a987	TYPNEPEAKLWKRIA AAKILSLLPIESSLX	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTTAAATT TA CGGGAAAAAG ACCCGTTTT

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51 AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACCGGAGC TGTCGATTAC GGAAGacgag tATGTCTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggcAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTGG TCAAAATGccg Cctcgaggcg
301 catAAAgAcg gtttcggctt cgcCGTCCGG CTCATGCCGA TGGACGAAGG
351 GGATTTCGTT TTATACGAAC GCCAgatgcg tggTGTcatG CACggcgaca
401 ccgttACCGT CCCCTCCTGCg ggtatggaaCC GCAGGGGccg ccgcGAAGgg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TC GGCGCTTT
501 CTATATGGAT AGGGGCGTGG CGATTTGGA GCCGGAAGAC AAGCGCTGTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG CAAAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAT cgAAATTGCG GTGCGCAAGC ATCATTGCG GCAccgaTTC
751 AGTGaagcgt gtGcCAAATC CGcgaAAAA ATtcccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTGACG ACGGCGTGTG TGCCGAAAAAA
901 CTCGGACGCA ATTACCGCCT GTGCGTGGCG ATTGCGGATG TCAGCCATT
951 TGTCGCCCT GACGATGCGA TTGATGCGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTG CTCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCAGTGC GAGCCTTTGT GTATGGTGTG
1101 CGATATGGTC CTTACCTATG CGGGCAATAT CAAGAAATAC CGTTCTATC
1151 CGCCCGTGT GCGCTCTCAT GCCCCCTGAA CC... J...CCA AGTTGGAAA
1201 TGGCTTCAG ACGGCATCGG GAATCCGCAC AAAGGCCAAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAAA ACGTCGGCG CGCGGGCGG
1301 TGGAGTTGA AAGCGTCGAA ACCCAGATGA TTTGACGCA CAACGGCAAA
1351 ATCGAAAAAA TTGTCGGCGT CGTCCGCAAC gatGCCACA AGTGATTGA
1401 AGAATGTATG CTGGCGCGA ATGTTGCGC GGC GGATTTT CTGTGAAAA
1451 ACAAACATAC CGCAACCATT TGGGCCCCAC GCCGAAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGGACAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAAACATTCA
1601 AAGGCAGGCC GGATGCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCCG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTGGCTTA
1701 TGAAGCATAC GCCCACCTTA CCTCGCCCAT CGCGCCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAA GCGTATTGA ACCGGAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTT GGGCGTGCAT ACTTCGTTT GCGAACGCCG
1851 TGCGCAGCAT GCTGGCGCG ATGTTGAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGGTGAAT ATTTGAG GcaaattCtc cgggggtgtg
1951 gcaaatttg gaATATTGTC CACTTTGGAC GATATccata tcgacggct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCAGA CGCAGCGCA TCCGTTCAA TATGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGGCGAT TTGGATGATG GAAAATCGA
2151 CTTGTCCTA ATTGCCGGAG AAAGCGCGAG GCGGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGCGGGCGG GGAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAACAGC CCGATGCCG AAAGTAAGGG GAAGGGCGT
2301 GCGTCCGTT GCGGAATCGG GGAAAAGGC AAAGAAACCG GTTCCGATTAA
2351 AGGTCAAAAAA ACGGAAAGGC AAATCATAA

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This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

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1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVP SKIESL
51 ARELSITEDE YVFFERRLKA MARDGVQLIN RRGAVCAADK LDIVKCRVEA
101 HKDGFGEFAVP LMPMDEGDFV LYERQMGRVM HGDVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGFRYMD RGVAILEPD KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPV AKIIEVLDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDSL KGRV DLDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTS VYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KA QIDTLYKL FKILQKKRLA RGA VE FESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQQLGL LGLQLGGGDN PSPKDYAALA EOFGKGRPDAE LLOVMMRLSM
551 QQAVYEPHCE GHFGGLAYEAY AHFTSPIRRY PDLT VHRRAIK AVLNRKTYTP
601 NKS WQALGVH TSFCERRADD AGRDVENWLK TYYMRDKVGE IFE GKISRGV
651 ANFGIFVTL DIIHDLVHI SDLGEDYFN RPEIMAIECF RSGIRFNMGD
701 RVA VRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSRT
751 TAEKKTARCG KVRGRGPVAV AESGKKAKKP VPIVKKRKG KS.

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

m988.seq	(partial)
1	..ACAGTTCTGG ATATTGTCGA ACGCGCGAA AGCAAAGTGG TCGGCCGTTT
51	CTATATGGAT AGGGCGTGG CGATTGGA GCGGAAGAC AAGCGTCTGA
101	ACCAAAGCAT CGTATTGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151	TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTATCCTG AGCAAAACCG
201	GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251	GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGCC GCACCAATTG
301	AGTGAAGCGT GTGCCAAAGC TGCAGAAAAA ATTCCCGTCC ATGTACGCAA
351	AAGCGATTG AAAGGCCGG TCGATTGCC CGACCTGCC TTGGTAACGA
401	TAGACGGCA AACGGCGC GATTTCGACG ACGGGGTGTG TGCCGAAAAA
451	GTCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
501	TGTCCGCCCT GACGATGTGA TTGATGCCAGA TGCTCAAGAA CGCAGTACCA
551	GCGTATATTG CCCCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601	AACGGCATTT GCTCGCTAA TCCCAGATGTC GAGCGTTTGT STATGGTGTG
651	CGATAATGGTC GTTACCTATG CGGGCAATAT CAAAGAACAT CGCTTCTACC
701	CCGCCGTAAT GCGCTCTCAT GCCCCCTGAA CCTACAACCA AGTTTGGAAA
751	TGGATTTCAAG CGGGCATCGA CCATCCGTAC AAAGCCAAA TCGACACCCCT
801	TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCG
851	TGGAGTTGAA AAGCGTCGAA ACCCAGATGA TTTCGATGA CAACGGCAAA
901	ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACAGCTGATTGA
951	AGAATGTATG CTGGCGCGA ATGTTGCGC AGCGGATTTC CTGTTGAAAA
1001	ACAAGCATAAC GGCTTTGTC CGCAACCATG TGGCCCCCAC GCGGAAAAA
1051	CTCGCCACCC TGCAGCGAGCA GCTCGGTCTG TTGGGCTTC AACTTGGCG
1101	CGGGGACAAAC CGTCGCCGA AAGACTATGCG CGCGCTTGTG GAAATTCA
1151	AAGGCAGACC TGATGCCGA TTGCTGCAAG TCATGATGTT CGCGCTCATG
1201	CAGCAGGGCG TTTACGAACC GCATTGCGAC GGACACTTTG STCTTGCCTA
1251	CGAAGCATAAC GCCCCACTCA CCTCGCCCAT CGGGCGCTAT CCCGACCTGA
1301	CCGTACACCG CGCCATCAAA GCGTGTGATGA ATCAGCAAAC CTACACGCCA
1351	AAAAAAAGCT GGCAGGCTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401	TGCGGACGAC GCCAGCCCG ACGTGAAAAA CTGGCTGAAA ACCTATTATA
1451	TGCGCGATAAA GGTCGGCGAA GTATTGCAAG GTAAAATCTC CGGCATGACC
1501	AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551	GCATATCAGC GATTGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
1601	TGGCAATCGA AGGCAGAACGC AGGCCATCC GTTCAACAT GGGGGACAGG
1651	GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATT
1701	TGTCCGTGATT GCGGGGGGAA CGGGCAGGGG CGGGAAAGTT AAATCATCCG
1751	CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGAAAGCC GAAAACCGCC

1400

1801 GCCGAGAAAAA AAACAGCCCCG AGGCCGGAAA GTAAGGGGAA GGGGCGCGTC
1851 TGCCGCCGCA GAATCAGGGA AAAAGGCAAA GAAACCGGTT CCGATTAAAGG
1901 TAAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

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Pcp (partida)
1 ..TVLIVEDERAQ SKVVGFRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEONRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
101 SEACAKAAKK IPVHVRKSDL KGRVLDRLDP LVTIDGETAR DFDDAVFAEK
151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTS VYFP RR VIPMLPENLS
201 NGICSLNPDV ERLCMVCMDV VTYAGNIKEY FFVPAVMRSH ARLTYNQWK
251 WISDGIDHPY KAQTDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
301 IEKIVPVVRN DAHKJ IEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
351 LATLREQLGL LGLQLGGDN PSPKDYAALV EQFKGRPDAE LLOVMMRLSRM
401 QQA VYEPHC D GHFGLAYEAY AHFTSPIRY PDLT VHRAIK AVLNQQTYP
451 KKSWQALGVH TSFCERRADD ASRDVENWLK TYYMRDKVGE VFEGKISGM
501 SFGIFVTLDG IHIDGLVHS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKTA
601 AEKKTARGGK VRGRGASA A ESRKKAKKPV PIKVKKRKGK S*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/q988 94.2% identity in 642 aa overlap

m988.pep			10	20	30
g988	LYERQMRGVMHGDVTVRPAGMDRRGRREGTFLDIVERAQS	KVVG	TVLDIVERAQS	KVVG	RFYMDRGVAILEPED
	130	140	150	160	170
m988.pep	40	50	60	70	80
g988	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKI	I	EVLG	DGYADSGMEIEIA	90
	190	200	210	220	230
m988.pep	100	110	120	130	140
g988	VRKHHLPHQFSEACAKAACKIPVHVRKSDLKG	RVDLPLVTIDGETARD	FDDAVFAEK	150	
	250	260	270	280	290
m988.pep	160	170	180	190	200
g988	VGRNYRLVVVAIADVSHYVRPDDVIDADAQERSTS	YFPRRVIPMLPENLSNGICSLNPDV	210		
	310	320	330	340	350
m988.pep	220	230	240	250	260
g988	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLT	YNQVWKWISDGIDHPYKAQIDTL	LYKL		
	370	380	390	400	410
m988.pep	280	290	300	310	320
g988	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRND	AHKLIECMLAANVCAADF	330		
	430	440	450	460	470
m988.pep	340	350	360	370	380
g988	LLKNKHTALFRNHLGPTPEKLATLREQLGLGLQ	LGGGDNPSPKDYAALVEQFKGP	RDAE		
	LLKNKHTALFRNHLGPTPEKLATLREQLGLGLQ	LGGCDNPSPKDYA	390		

1401

	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
g988	LLQVMMRLSRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRYPDLTVHRAIKAVLNQQTYP 550	560	570	580	590	600
m988.pep	460	470	480	490	500	509
g988	KKSWQALGVHTSFCERRADDASRDVENWLKTYYMRDKVGEVFEGKIS-GMTSFIFVTLD 610	620	630	640	650	660
m988.pep	510	520	530	540	550	560
g988	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL 670	680	690	700	710	720
m988.pep	570	580	590	600	610	620
g988	IAGGSGRGRKVKSASAKPAGTAGKGPKTAEEKKTARGGKVRGRGASAAAESRKKA 730	740	750	760	770	780
m988.pep	630	640	VPIKVKKRKGSX			
g988		VPIKVKKRKGSX				
		790				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

a988.seq	1 ATGAATAAAA ATATTAAATC TTTAAATT TA CGGGAAAAAG ACCCGTTTT
	51 AACTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGAAATGGA
	101 TAATCGAGCT GCTTGAACGT AAAGGCCTAC CATCCAAGAT TGAAGCTTTG
	151 GTACCGAAT TGTCGATTA GGAAGAAGAG TACGAATTT TCAGAACGTCG
	201 TCTGAAGGCG ATGGCCGGG ACGGTCAAGT TTAAATCAC CCGTCGGGGCG
	251 CGGTTGCGC CGGCCACAAA TTGGATTGG TCAAATGCCG TGCAAGGCCG
	301 CACAAGACCC GCTTCGGTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
	351 TGATTTGTC TTGTACGAAC GCCAGATCG CGGCATTATG CACGGCGATA
	401 TTGTCACTGT TCGTCTGCC GGCATGGACG GTAGGGCCG CGCGAAGGG
	451 ACGGTTCTGG ATATTGTCGA ACGCGCCAA AGCAAAGTGG TCGGCCGTT
	501 CTANATGGAT AGGGCGTGG CGATTTGGA CGCGGAAGAC AAGCGTCTGA
	551 ACCAAAGCAT CGTATTGAA CGGGACGGCG TGGCGCGTTT CAAACCTGAA
	601 TCCCGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAACCG
	651 GCGGGCAGTG CAAAAATCA TCGAAGTTT GGGCGATTAT GCGACAGCG
	701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGCG GCACCAATTG
	751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
	801 AAGCGATTG AAAGGCCCGC TCGATTGCG CGACCTGCCT TTGTTAACGAA
	851 TAGACGGCGA AACCGCTCGA GATTTGACG ATGCGGTGTT TGCCGAGAAA
	901 ATCGGACGCA ATTACCGTCT GGCGTGGCG ATTGCCGATG TCAGCCATTA
	951 TGTCCGCCCG GATGACCGCTA TCGACACCGA CGCTCAGGAA CGCAGCACCA
	1001 GTGTTTACTT CCCGCCCGC GTGATTCCA TGTTGCCCGA AAACCTGTCC
	1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCCTTGT GTGTTGTGTG
	1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
	1151 CGCCCGTGAT GCGCTCTCAT GCGCGCTGA CCTACACCA AGTTGGAAA
	1201 TGGCTTCAG CGGGCATCGA GCATCCGTC AAAACCCAAA TCGACACGCT
	1251 TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGCGG
	1301 TGGAGTTGA CAGCATCGA ACCCAAATGC TTTTCGACGA CAACGGTAAA
	1351 ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACAGCTGATTGA
	1401 AGAATGTATG TTGGCGGCAA ACGTTTCGCG AGCGGATTTT CTGTTGAAAAA
	1451 ACAAGCATAC CGCATTGTC CGCAACCATT TGGGGCCAC GCGCGAAAAAA
	1501 CTCGCCGCCT TCGCGCAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
	1551 CGGCGACAAAC CGCTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
 1651 CAACAGGCCG TTTACGAACC GCATTGCGAC GGACACTTG GTCTTGCCTA
 1701 CGAACATAC GCCCACTTC CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
 1751 CCGTACACCG CGCCATCAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
 1801 AAAAAAAGCT GGCAGGCTTT GGGCGTCAT ACCTCGTTCT GTGAGCGCCG
 1851 TGCGGACGAC GCGAGCCGAC ACCTGGAAAA CTGGCTGAAA ACCTATTATA
 1901 TGCGCGATAA GTCTGGCGAA GTATTGAGA GTAAAATCTC CGGCATGACC
 1951 AGTTTGGTA CTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
 2001 GCATATCAGC GATTGGCGC AAGACTATT CAACTCCGC CCCGAAATCA
 2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
 2101 GTTGCCTGTC GGGTCGCCCC TGCCGATTG GATGACGGAA AAATCGATT
 2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
 2201 CGCTCTGCAA ACCGGCAGGG ACCGGCGGGGA AAGGAAAGCC GAAAACCGCC
 2251 GCGGAGAAAA AACAGCCCG AGCGGGCAAA GTAAGGGGAA GGGGCGCGTC
 2301 TGCCGCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 2351 TAAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pep
 1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVP SKIEAL
 51 VRELSIKEEE YEFFERRLKA MARDQQLIN RRGAVCAADK LDIVKCRVKA
 101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HDIVTVRPA GMDGRGRREG
 151 TVLDIVERAQ SKVVGRCXMD RVVAILEPED KRLNQSIVLE PDGVARFKPE
 201 SGQVIVGEIE VYPEQNRPAV AKIIIEVLGDY ADSGMEIEIA VRKHHLPHQF
 251 SEACAIAKK IPDHVRKSDL KGRVDLRDLPLVTIDGETAR DFDDAVFAEK
 301 IGNRYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFPRR VIPMLPENLS
 351 NGICSLNPV ERLCVVCDMV ITYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFEDSIE TQMLFDDNGK
 451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAE LLQVMMRLSM
 551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYTP
 601 KKSWQALGVH TSFCERRADD ASRDVENWLK TYYMPDKVGE VFECKISGMT
 651 SFGIFVTLGD IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 701 VAVRVARADL DDGKIDFVLI AGGSGRGRKVV KSSASAKPAG TAGKGKPKTA
 751 AEKKTARGKK VRGRGASAAA ESRKKAKKPV PIKVKKRKKGK S*

m988/a988 97.0% identity in 641 aa overlap

		10	20	30			
m988.pep		TVLDIVERAQSKVVGRCXMDRVGAILEPED					
a988	LYERQMRGIMHDIVTVRPAGMDGRGRREGTVLDIVERAQSKVVGRCXMDRVGAILEPED	130	140	150	160	170	180
m988.pep	KRLNQSIVLEPDGVARFKPESGQVIVGELEVYYPEQNRPAVAKIIEVLGDYADSGMEIEIA	40	50	60	70	80	90
a988	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYYPEQNRPAVAKIIEVLGDYADSGMEIEIA	190	200	210	220	230	240
m988.pep	VRKHHLPHQFSEACAKAKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK	100	110	120	130	140	150
a988	VRKHHLPHQFSEACAKAKIPDHRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK	250	260	270	280	290	300
m988.pep	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTS VYFP RRVIPMLPENLSNGICSLNPDV	160	170	180	190	200	210
		:					
a988	IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTS VYFP RRVIPMLPENLSNGICSLNPVH	310	320	330	340	350	360
m988.pep	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL	220	230	240	250	260	270
a988	ERLCVVCMDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLGGIEHPFKTQIDTLYKL						

1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988						
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQQLGLQLGGGDNPSPKDYAAALVEQFKGRPDAE					
a988						
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLOVMMRLSRMQQAVYEPHCDGHFGLAYEAYAHFTSPIRYPDLTVHRAIKAVLNQQTYTP					
a988						
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSWQALGVHTSFCCRADDASRDVENWLKTYYMRDKVGEVFEKGKISGMTSFGIFVTLDG					
a988						
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988						
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSASAKPAGTAGKGKPKTAAEKKTARGKVRGRGASAAAESRKAKKPV					
a988						
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGKSX					
a988						
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq	1 ATGACCCCTT TCACACTGAA AAAAACGTC CTGCTGCTCG GCACTGCCTT
	51 TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
	101 TCAACGCGCA AAGCACGGCA AATGCCGCG ACGCCTCGAC CATCTTCTAC
	151 AATCCCAGCG GCCCTGACCAA ACTCGACAGC AGCCAGATT CCCTCAACGC
	201 CAACATCGTG CTGCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
	251 TTACCGGGCT TCCCGTCAA GGTTCTAAAA AGCGCAAAAT CACCAAAACC
	301 ACGGTCGCAC CCCACATT TA CGCGCATAC AAAGTCAACG ACAATCTGAC
	351 CGTGGGCTTG GCGCTGTACG TCCCCCTCGG CTCTGCCACC GAATACGAAA
	401 AAGATTCCGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
	451 GCCGTCGAAC CTGTCGCCGC GTGGAAACTC AACGAACGCC ATTCCCTCGG
	501 CGCAGGCATC ATCGCCCAAC ATAATCCGC CGAACTGCGC AAATATGCCG
	551 ACTGAGGAAT CCCAAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
	601 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAGG
	651 CAGCGATTGG GCGCTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
	701 ACCGCGCGCG CGTGGCGTGT AACTACCGTT CCAAAGTTTC ACACACGCTC
	751 AAAGGCGATG CGGAATGGGC GGCAGACGGC GCGGCGGGA AACAAACAGTG
	801 GAATGACAAT ATGCTCACAC CGCTCGGT A CAGGGGAAT GAAAAAGCCA
	851 GTGTAAAAAT CGTAACGCCCT GAGTCTTGT CGTACACGG CAGTACAAA

```

901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACTTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTGAA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAAA ATCCGACCAC ACCACCATCA CCCCCAACTG GCGAACACCC
1051 TACAAAGTCG GCTTGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAAACGCC TGTCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGCTTCTC CGCCGGCATG
1201 AAATACCCATA TCGGCAAAAA CCACGTGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

g989.pep

```

1 MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHYIGAY KVNDNLTVCL GVYVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAQAQIKAD GHADVKGSWD GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQOWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMYK
301 VSDKADLFBD VTWTRHSRFN KAELFFEKEK NIANGKKSDR TTITPNWRNT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHV DAAVTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

m989.seq

```

1 ATGACCCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCCGCGCA TCCGTCCACG CATCCGGCTA CCACCTCGGC ACACAGTCGG
101 TCAACCGCGCA AAGCACCGCA AATGCCGCCG CGCGAGAACG CGCCGACGCA
151 TCGACCATCT TCTACAAACCC TGCCGGCTCG ACCAAACTCG ACAGCAGCCA
201 GATTCCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCTAT TATGAGGCGG
251 ATTCCCGGAC CGACTTTACC GGGCTTCCCG TCCAAGGTTTC GAAAAGCGGC
301 AAAATCACCA AAACCACCGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGCGT GTACGTCCCC TTCCGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTGTC GGCACAAACAT CAACAAACTC
451 GGTCGTGACCA GCATCGCCGT CGAACCTGTC GCGCGTGGAA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCCGCGAAC
551 TGGCCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAAGGC
651 CGACGGACAC GCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACATAC
751 CGTTCGAAAG TCTCGCACAC GCTCAAAGGC GATGCGGAAT GGGCGCGAGA
801 CGGCGCGCGC GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACCGCGAA TGAAAAAGCC CGCGTTAAAAA TCCTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGA
951 CGTAACCTGG ACACGCCACA GCGCCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAGAAAAA ACCCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAAGTGGC GCAACACCTA CAAAGTCGGC TTCCGGGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC CGCGCGGCAT CGCTTTGAC AAATCGCCCG
1151 TCCGCAACCGC CGACTACCGC ATGAAACAGCC TACCCGACGG CAACCGCATE
1201 TGGTTCTCG CCGGTATGAA ATACCATATC GTGAAAAAAC ACCTCGTGA
1251 TGCCGCTAC ACCCACATCC ACATCAACGA CACAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

m989.pep

```

1 MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYVNND LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAEILRKYADW GIKSKAEILT
201 AKPPPKNGVA EAAKIQFDGH ADVKGSDWGF GYOLAWMWDI NDRAVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGTYANEKA RVKIVTPESL
301 SVHGMYKVSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

```

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNI
 401 WFSAGMKYHI GKNHVVDAAY THIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

g989.pep	10 20 30 40 50
	MTPFTLKKTVLLLTAFAAAAVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL
m989	10 20 30 40 50 60
	MTPSALKTVLLLTAFAAAAVHASGYHFGTQSVNAQSTANAAAEEAADASTIFYNPAGL
g989.pep	60 70 80 90 100 110
	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN
m989	70 80 90 100 110 120
	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
g989.pep	120 130 140 150 160 170
	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAWKLNERHSFGAGIIAQHN
m989	130 140 150 160 170 180
	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAWKLDRHSFGAGIIAQHT
g989.pep	180 190 200 210 220 230
	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI
m989	190 200 210 220 230 240
	SAELRKYADWGIKSKAEILTAKPPKPNVVAEAKI QADGHADVKGSDWGFHYQLAWMWDI
g989.pep	240 250 260 270 280 290
	NDRARGVNVYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES
m989	250 260 270 280 290
	NDRARGVNVYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES
g989.pep	300 310 320 330 340 350
	LSVHGMVKVSDKADLFGVTWTRHSRFNKAELFFEKEKNIANGKSDRTTITPNWRNTYK
m989	300 310 320 330 340 350
	LSVHGMVKVSDKADLFGVTWTRHSRFDKAELVFEKEKTVVKKGK-SDRTTITPNWRNTYK
g989.pep	360 370 380 390 400 410
	VGLGGSYQISEPLQLRGIAFDKPPVRNADYRMNSLPDGNIWFSAGMKYHIGKNHVDA
m989	360 370 380 390 400 410
	VGFGGSYQISEPLQLRGIAFDKSPVRNADYRMNSLPDGNIWFSAGMKYHIGKNHVDA
g989.pep	420 430 440 450 460
	AYTHIHINDTSYRTAKASGNVDVDSKGASCARFKNHADIIGLQTYKFKX
m989	420 430 440 450 460
	AYTHIHINDTSYRTAKASGNVDVDSKGASSARFKNHADIIGLQTYKFKX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq

1	ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT
51	TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
101	TCAACGGCGA AAGCACGGCA AATGCCCGCG CGCGAGAACG CGCCGACGCA
151	TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201	GATTCCGTC AACGCCAACA TC GTGCTGCC CAGCATT CAT TATGAGGCCG
251	ATTCCGCCAC CGTCTTACC GGGCTTCCCG TCCAAGGTTTC GAAAAGCGGC

301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATAACAAAGT
 351 CAACGACAAT CTGACCGTAG GCTTGGCGT GTACGTCCCC TTGGTTCTG
 401 CCACCGAATA CGAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
 451 GGCTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGG AACTCAACGA
 501 ACGCCATTCC TTCCGGCGCA GCATCATCGC CCAACATACT TCCGCGGAGC
 551 TGCGCAAATA TGCGGACTGG GGGATTATGG AAAAGCGAA AGCACTAAAA
 601 GAAACACCCCC CCAATCAAC TAAAGCGGCC CAAATCAAAG CCGACGGACA
 651 CGCCGATGTC AAAGGCGAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGG
 701 TGTGGGACAT CAACGACCGT GCGCGCTGG GCGTGAACTA CGCTTCAAA
 751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGGCGAG ACCACGCAAT
 801 GGCAGAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
 851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTGTCCTGTA
 901 CACGGTATGT ACAAAAGTGTG CGACAAAGCC GACCTGTTCG GCGACGTAAC
 951 TTGGACGCGC ACAGCGCGT TCGATAAGGC GGAACCTGGTT TTGAAAAAG
 1001 AAAAACCAT CGTCAACGGC AAATCCGAC GCACCAACAT CACCCCCAAC
 1051 TGGCGCAACA CCTACAAAGT CGGCTCGGC GGTTCTTATC AAATCAGCGA
 1101 ACCGCTGCAA CTGCGCGCC GCATCGCTTT TGACAAATCG CCCGTCGCA
 1151 ACGCCGACTA CCGCATGAAC AGCCTGCCG ACGGCAACCG CATCTGGTTC
 1201 TCCGCCGGCA TGAAATACCA TATCGCAAA AACACGTCG TCGATGCCGC
 1251 CTACACCCAC ATCCACATCA ACACACCCAG CTACCCACG GCGAAGGCAA
 1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCGGCACG TTCAAAAAC
 1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

a989.pep

```

1 MTPSALKKTV LLLGTAFAAA SAQASGYHFG TGSVNAOSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISVN NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAEELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGSDWGFGYQ LAWMWDINDR ARVGVNRYSK
251 VSHTLKGDAAE WAADDAMAKQ LWADNKALL GYTPSEKARV KIVTPESLW
301 HGMYKVSDKA DLFGDVTWTR HSRFDKAELV FEKEKITIVNG KSDRTTITPN
351 WRNTYKVGFQ GSQIPIEPLQ LRGIAFDKS PVRNADYRMN SLPDGDNRIWF
401 SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASQNDVDS KGASSARFKN
451 HADIIQLQYT YKFK*
  
```

m989/a989

93.1% identity in 467 aa overlap

m989.pep

10	20	30	40	50	60
----	----	----	----	----	----

a989

10	20	30	40	50	60
----	----	----	----	----	----

m989.pep

70	80	90	100	110	120
----	----	----	-----	-----	-----

a989

70	80	90	100	110	120
----	----	----	-----	-----	-----

m989.pep

130	140	150	160	170	180
-----	-----	-----	-----	-----	-----

a989

130	140	150	160	170	180
-----	-----	-----	-----	-----	-----

m989.pep

190	200	210	220	230	240
-----	-----	-----	-----	-----	-----

a989

190	200	210	220	230	
-----	-----	-----	-----	-----	--

m989.pep

250	260	270	280	290	299
-----	-----	-----	-----	-----	-----

a989

250	260	270	280	290	299
-----	-----	-----	-----	-----	-----

1407

	240	250	260	270	280	290	
m989 . pep	300	310	320	330	340	350	359
	LSVHGMYKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGKSERTTITPNWRNTYKV						
a989	300	310	320	330	340	350	
	LSVHGMYKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGKSERTTITPNWRNTYKV						
m989 . pep	360	370	380	390	400	410	419
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA						
a989	360	370	380	390	400	410	
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA						
m989 . pep	420	430	440	450	460		
	YTHIHINDTSYRTAKASGNDVDSDKASSARFKNHADIIGLQYTYKFKX						
a989	420	430	440	450	460		
	YTHIHINDTSYRTAKASGNDVDSDKASSARFKNHADIIGLQYTYKFKX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

m990 . seq	1	ATGTTCAAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCCA
	51	CGATGCCGAT TTTTCATTTC CAGACAAGCC GAAAACCGGC ACTTCCCATT
	101	ATTTTCCAG CGGTAAAACC GATCAAATT CATCGAATA TGCGTATGAC
	151	GAAATCAATA TCCAAGGTAA AAATTACAAT AGCAGCATCC TCGCCGTGCA
	201	TAATATGCCG GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
	251	TAAAGCAGGC GGTTAAAAGT CAATTACAGG ATTATACAAA ACAAGACCG
	301	GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCCT ATATAGCAC
	351	GTGTTGAAACA AAATTTAGTA CGCTAACAA GACGATGCC GATTTAATT
	401	ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
	451	ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
	501	CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
	551	AAGATTCCCT TTGGGAACCG CGCCGCCATT CGCACATCCA TACGCTGGAA
	601	ACTTCCGATA ATGCCCGCAT CGCCCTGAAC ACGAAAGATG AAAAACTGAC
	651	CGTCCATAAG GATTATGCCG CGGGCGCGGA TTTCTGTTG GCCTACGACG
	701	TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
	751	CAATCCGGCG TGGTTTGGGA ACGCCGCCG GAAAATCTGA AAACGCTCGA
	801	CGGGCGCAAAC CTGATTGCCG CAAAAACGGC GGATTCGGT TCGTTTGCCT
	851	TTAACACAAA TTACCGCGAG GGACTGTACG ATTATTTGCT CAAAGCAATGC
	901	GAAGGCGGAT TTTGTTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
	951	AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGC
	1001	TGCGTCCCGC CGACAGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
	1051	CAAAATTGT GGCTCGCTT CATCGCCGGC CGGTGCGCATC AAAATATACG
	1101	GGGCAGCGCG GCTCGCGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGCG
	1151	AGGTGTTGT ACGGCAAAT GAAGGCAGCC GACTGGCAAT CGCGTGTATG
	1201	GGCGGCAGGG CCGGCCAGCA CGCATCGTC AACGGCAAAG CGCGTGCAGC
	1251	AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TTGTTATGCT CGCTGGCATC
	1301	AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCATAC
	1351	CAACGTTCA AACACCGCAT CAATGATGAA AACCGTGCAG AACGCTACAA
	1401	AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
	1451	CGGAAGGCAT TGTCGAAAGA GGCAATAATG TGCGGTTTA CCTACAACCG
	1501	CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGGCGCTTTA CGCACAGCGA
	1551	GGGGACGGCG GTCCGACTGC TCAGGAGCGG TCAGTGGCAA AGCCCGCGCG
	1601	GCATTCCGGC AAAAACCCGT TTTGCTTGC GTAACGGTGT CAATCTTCAG
	1651	CCTTTGCGC CTTTAATATGT TTTGACAGG TCAAAATCTT TCGCGTGGG
	1701	AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
	1751	GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
	1801	TATGGCAAAA GGACGGACGG CGACAAAGAA GCGCATTGT CGCTCAAATG
	1851	GCTGTTTGA

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990 . pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWEENKKRT EEAYIEQLGP KF~LKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK AYQQYAAQFTG KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
251 QSGVVLERRP ENLKTLGGRK LIAAKTADSG SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQYAAQFTG LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRILAIGVM
401 GGRAGOHASV NGKGGAAAGSD LYGYGGVVA AWHQLRDKQT GAYLDGWLQY
451 ORFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNVRFYLQP
501 QAQFTYLGVN GGFTDSEGT A VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LCCRGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLE*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTCAAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCCA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCAT
101 ATTTCCTCAG CGGTAAAACC GATCAAAATT CATCCGAAATA TGTTATGAC
151 GAAATCAATA TCCAAGGTA AAACATACAAT AGCAGGCATAC TCGCCGTCGA
201 TAATATGCC C GTTGTAAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTATACAA ACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCCT ATATAGAAC
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATT
401 ATAATTTGGT AGAAGATTCC GTACTCTAC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA AACACATCTT CAATAAAAAA TTACACGTCA AAATCGAAA
501 CAAATCCCAC GTCGCCGAG ACAGTGTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCTT TTGGGAACCG CGCCGCCATT CGCAGATCCA TATGCTGGAA
601 ACTTCGATA ATGCCCGCAT CGGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTTGGA ACAGCCGGCC GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAAATACT TTGTTGGGC
1001 TCGCTGCCGC CGACAGGGC GACGACGTGT ATGCCGCCGA TCCGTCCTCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGCCGGC CGGTGCGCATC AAAATATACG
1101 GGGCGGCGCG GCTCGGGACG GCGGGCGCAA AGGCGTGCAA ATCGGCGGCC
1151 AGGTGTTTGT ACAGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GCGGGCAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TTGTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCAG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTCGAAAAGG CGCAATAATG TGCGTTTTA CCTGCAACCG
1501 CAGGCAGCAGT TTACCTACTT GGGCGTAAAC GCGGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCAGGCGAGG TGAGCTGGCAA AGCCGCGCCG
1601 GCATTGGGC AAAACCCGT TTTGCTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCT CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGG
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCGCATTGT CGCTCAAATG
1851 GCTGTTTGAA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKKYITDTY GDNLKDAVKK QLQDLYKTRP
101 EAWEENKKRT EEAYIEQLGP KF~LKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK AYQQYAAQFTG KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
251 QSGVVLERRP ENLKTLGGRK LIAAEKADS SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQYAAQFTG LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRILAIGVM

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401 GGRAGQHASV NGKGGAAQSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
 451 QRFKHRINDE NRAERYTKG WTASVEGGYN ALVAEGVVGK GNVRFYLQP
 501 QAQFTYLGVN GGFTDSEGT A VGLLGSGQWQ SRAGIRAKTR FALRNGVNLO
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
 601 YGKRTDGDKE AALSLKWLF.

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTQNSSEYGYDEINIQGKNYN					
	10	20	30	40	50	60
m990.pep	70	80	90	100	110	120
a990	SGILAVDNMPVVKKYITEKYGADLKQAVKSQLODLYKTRPEAWAENKKRTEEAYIAQFGT					
	70	80	90	100	110	120
m990.pep	KFSTLKVQMPDLINKLVEDSVLTPHSNTSQTSLNNI FNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNI FNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
m990.pep	MTLKDSLWEPRRHSDIHLTSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDKP					
	190	200	210	220	230	240
m990.pep	ALTFEDKVSGQGVVLERRPENLKTLDGRKLIAAKTADSGSFQAFKQNYRQGLYELLKQC					
a990	ALTFEEKKVSGQGVVLERRPENLKTLDGRKLIAAEKADSNSFAFKQNYRQGLYELLKQC					
	250	260	270	280	290	300
m990.pep	EGGFCLGVQRЛАIPEAEAVLYAQQAЯANTLFGLRAADRGDDVYADPSRQKLWLRFIGG					
a990	EGGFCLGVQRЛАIPEAEAVLYAQQAЯANTLFGLRAADRGDDVYADPSRQKLWLRFIGG					
	310	320	330	340	350	360
m990.pep	370	380	390	400	410	420
a990	RSHQNIRGAAADGWRKGVQIGGEV FVRQNEGSRLAIGVMGRAGQHASVNGKGGAAAGSD					
	370	380	390	400	410	420
m990.pep	LYGYGGGVYAAWHQLRDQQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHG YGGGVYAAWHQLRDQQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
m990.pep	ALVAEGIVGKGNVRFYLQPQAQFTYLGVNNGFTDSEGTAVGLLGSGQWQS RAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQPQAQFTYLGVNNGFTDSEGTAVGLLGSGQWQS RAGIRAKTR					
	490	500	510	520	530	540
m990.pep	FALRNGVNLOPFAAFNVLHRSKSFGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLOPFAAFNVLHRSKSFGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
	550	560	570	580	590	600

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	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

g992.seq

1	ATGTTCAAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAATCAT
51	GAAATGGCTT CCCGTGCCG TGTCGCTTT GGGCGCGTTG GGTTATACGG
101	GATATGACAG TGAGGCCTG CGGACGGCGG TTGCGTACT CGACGTTACTC
151	GGCACTGCAG GGGACGTTGGG TTTCGACGCC CCGCTTCGCC GACGGGCATC
201	GGCAGAACATCC GGCCACAGCT ACACAGGCAC GGTGTCACAA GTCTATGACG
251	GCGATACCTT TCACGTCATC GACGGCAGAC GCGCGAAACA TAAAATTCGG
301	ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTTC
351	CGCCGACAACT CGTCGCGCCG CGGGCGAGGG TAGGAAAGTC TGTACGTTG
401	TGTTTGAAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCCGGC
451	AAAACCGATT TGAACCTGAT GCAGGTGCAAG GACGGGGCGG CGTGCCTTAA
501	TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGGGATTTC GCGACTATG
551	CCGACGCTCA AATTCAAGGGCG GAAAGGGAAAC GCAAAGGATT GTGAAAGCT
601	AAAAATCCGC AAGCGCCGTG GGCCTACCGC CGGGCAGGCA GGAGCGGGCGG
651	GGGCAATAAG GATTGGATGG ATTCCGTGGG CGAATGGTTG GGCATTGGT
701	AA

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

g992.pep

1	MFRRRHRLKN MQIKKIMKWL PVALSLLGAL GYTGYDSEAV RTAVAVLDVL
51	GTAGDVGFD A PVRRRASAKS GHSYTGTVSK VYDGDTLHVI DGDGAKHHKIR
101	MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151	KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA
201	KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

m992.seq

1	ATGTTCAAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAATCAT
51	GAAATGGCTT CCCGTGCCG TGTCGCTTT GGGCGCGTTG GGTTATACGG
101	GGTACGGCAG CGAGGCCGTG CGGACGGCGG TTGCGTACT CGACGTTACTC
151	GGCGCGGAG GGGACGCGGG TTCCGACGCC CCGCCCGCC GCCGAGCATC
201	GGCAGAACATCC GGCCACCGCT ACACAGGCAC GGTGTCACAA GTCTATGACG
251	GCGACACCTT TCACGTTATC GACGGCAGCG GCGCGAAACA CAAAATCCGG
301	ATGGCGTATA TCGACGCCGG CGAGATGAAA CAGGCTTACG GCACGGCTTC
351	CGCGCAGAAC CTGCGCGCCG CGGGCGAAGG CAGGAAAGTC AGCGTSCGCG
401	TGTTCGATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGGC
451	AAAACCGATT TGAACCTGAT GCAGGTGCAAG GACGGGGCGG CGTGCCTTAA
501	TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGGGATTTC GCGATTATG
551	CCGACGCTCA AATTCAAGGGCG GAAAGGGAAAC GCAAAGGATT GTGAAAGCT
601	AAAAATCCGC AAGCGCCGTG GGCCTACCGC CGAGCAGGCA GGAGCGGGCGG
651	GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701	AA

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

m992.pep

1	MFRRRHRLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
51	GAAGDAGSSDA PARRRASAKS GHRYTGTVSK VYDGDTLHVI DGDGAKHHKIR
101	MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSVG
151	KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA
201	KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

	10	20	30	40	50	60
m992.pep	MFRRHRHLKNMQIKKIMKWLPVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA 					
g992	MFRRHRHLKNMQIKKIMKWLPVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA 10 20 30 40 50 60					
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGTISKVYDGDTLHVI DGDGAKHKIR MAY IDAPEMKQAYGTRSRDN 					
g992	PVRRRASAKSGHSYTGTISKVYDGDTLHVI DGDGAKHKIR MAY IDAPEMKQAYGTRSRDN 70 80 90 100 110 120					
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFETDRYQREVAQSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF 					
g992	LRAAAEGRKVSVRVFETDRYQREVAQVSAGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF 130 140 150 160 170 180					
	190	200	210	220	230	
m992.pep	ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX 					
g992	ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDSVGEWLGIWX 190 200 210 220 230					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

1	ATGTTCAGAC	GGCATCGGCA	TTTGAAAAT	ATGCAGATTAA	AAAAAAATCAT
51	GAAATGGCTT	CCCGTCGCCCT	TGTCGCTTT	GGGTGCGTTG	GGTTATACGG
101	GTTACGGCAG	CGAGGCCTTG	CGGACGGCGG	TTGCCGTACT	CGACGTACTC
151	GGCGCGGAG	GGGACGCGGG	TTCCGACCGG	CCCGCCCGCC	GGCGAGCATC
201	GGCGAAATCC	GGCCACCCTG	ACACAGGAC	GGTGTCCAAA	GTCTATGACG
251	GGCGACACCT	TCACGTTATC	GACGGCGACG	GGCGCAAACA	CAAATCCGG
301	ATGGCGTATA	TCGACGCGCC	GGAGATGAAA	CAGGCTTAGG	GAACCGCTTC
351	GGCGGACAAAC	CTGCGCGGG	CGGGCGAAGG	CAGGAAAGTC	AGCGTCCCGC
401	TGTTCGACAC	CGACCGCTAC	CAGTCCGAA	TGGCTTGGT	TTCTGTCCGC
451	AAAACCGATT	TGAAACCTGAT	GCAGGTGCGAG	GACGGGGCGG	CGTGGCATTAA
501	TAAAGTTAT	GCTAAAGAAC	AGCAGGATAAA	GGCGGATT	GGCGATTATG
551	CCGACGCTCA	AATTCAAGGGC	GAAAGGGAAAC	GCAAAGGATT	GTGAAAGCT
601	AAAATCCGC	AAGGCCCGTG	GGCGTACCGC	CGGGCAGGCA	GGAGCGGC
651	GGGCAATAAG	GATTGGATGG	ATGCCGTGGG	CGAATGGTTG	GGCATTTGGT
701	AA				

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

1	MFRRHRHLKN	MQIKKIMKWL	PVALSLLGAL	GYTGYGSEAV	RTAVAVLDVL
51	GAAGDAGSDA	PARRRASAKS	GHRYTGTISKV	VYDGDTLHVI	DGDGAKHKIR
101	MAYIDAPEMK	QAYGTRSRDN	LRAAAEGRKV	SVRVFDTDRY	QREVAQVSVG
151	KTDLNLMQVQ	DGAAWHYKSY	AKEQODKADF	ADYADAQIQA	ERERKGLWKA
201	KNPQAPWAYR	RAGRSGGGNK	DWMDAVGEWL	GIW*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRHRHLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA 					
m992	MFRRHRHLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA 10 20 30 40 50 60					
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGTISKVYDGDTLHVI DGDGAKHKIR MAY IDAPEMKQAYGTRSRDN 					
m992	PARRRASAKSGHRYTGTISKVYDGDTLHVI DGDGAKHKIR MAY IDAPEMKQAYGTRSRDN 70 80 90 100 110 120					
	130	140	150	160	170	180

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a992.pep	LRRAAEGRKVSVRVFDTDRYQREVAQSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF				
m992	LRRAAEGRKVSVRVFDTDRYQREVAQSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF				
	130	140	150	160	170
	190	200	210	220	230
a992.pep	ADYADAQIQAERERKGILWAKNPQAPWAYRRAGRSGGGNKKDWMDAVGEWLGIWX				
m992	ADYADAQIQAERERKGILWAKNPQAPWAYRRAGRSGGGNKKDWMDAVGEWLGIWX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

g993.seq

1	CTGAAAGTCG	TATTGGGCAG	TTTCAAGGC	CCTTGATC	TGCTGCTCTA
51	CCTTATCCG	AACAGAACAA	TCGATGTTCT	CGATATTCCG	ATGGTGAA
101	TTACCGGGCA	GTATCTGCC	TATATTGCC	AAATGGAAAC	CTATCAGTT
151	GATTGGGG	CGGAATATCT	TTTGATGGG	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCTG	CTGCTGCCG	GTACCGAAC	CGTCGAAGAC	GAAGAGGCG
251	ACCCGCGCTG	CGAGTTGGT	CGCCGCTCTC	TTGCCTACGA	GCAAATGAAA
301	CTGGCGCTGC	AGGGTTTGG	CGCGCTGCCG	CGTGCGGGAC	GGGATTTCG
351	CTGGGCTTAC	CTGCCGCTGG	AAATTGACG	CGAGACGAAG	CTGCCCGAGG
401	TTTACATCGC	CGATTGATG	CAGGCATGTT	TGGGCATTCT	TTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTAATCCAA	GAAACCCCTT	CCGTGCGCGC
501	GCAAATGACG	GAATCCTGC	GCCGTTGAA	CGAACACCGG	ATATGCAAGT
551	TTCACGCGCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GATCGTCAAC
601	TTCATCGCCC	TGTTGGAGCT	TGCCAAAGAA	GGATTGGTCG	GAATGTACA
651	GGAAGACGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAAGCGG	CATTTCCGC	ACACGGGGCG	GGCGCGATGT	CTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

g993.pep

1	LKVVLGSFQG	PLDLLLLYLIR	KQNIDVLDIP	MVEITGOYLH	YIAQMEAYQF
51	DIAEYLLMA	AMLIEIKSRL	LLPRTEAVED	EEADPRAELV	RRLLAYEQMK
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAAEFK	LPEVYIADM	QAWLGILSRA
151	KHTRSHHEVIQ	ETLSVRAQMT	AILRRLNEHG	ICRFHALFNP	EQGAAYVIVN
201	<u>FIALLELAKE</u>	<u>GLVGIVQEDG</u>	<u>FGEIRISLNH</u>	<u>EGAHS</u>	<u>DGIFG</u> TRGRDV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

m993.seq

1	TTGAAAGTCG	TATTGGGCAG	CTTCCAAGGC	CCTTGATC	TACTGCTGTA
51	TCTGATCCG	AAACAGAACAA	TCGACGTACT	GGATATTCCG	ATGGTGAA
101	T T A C C G A G C A	G T A T C T G C C A	T A C A T C G C C C	A A A T G A A A C	C T A T C A G T T
151	G A T T T G G C G G	C G G A A T A T C T	T T T G A T G C C A	G C A A T G C T G A	T T G A A A T C A A
201	A T C G C G C T G	C T G C T G C C G	G T A C C G A A C	C G T C G A A G A C	G A A G A G G C G
251	A C C C G C G T G C	C G A G T T G G T G	C G C C G C C T G C	T G G C T T A C G A	A C A G A T G A A G
301	C T G G C G C G C	A G G G T T T G G A	C G C G C T G C C C	C G A G C C G G A C	G G G A T T T C G C
351	G T G G G C T T A C	C T G C C G C T G G	A A A T T G C C G T	C G A A G C C A A G	C T G C C C G A A G
401	T C T A T A T T A C	C G A C T T G A C G	C A A G C G T G G C	T G G G T A T T T T	G T C T C G G G C A
451	A A A C A C A C G C	G C A G C C A C G A	A G T A A T C C A A	G A A A C C A T C T	C C G T G C G C G C
501	G C A A A T G A C G	G C A A T C C T G C	G C C G T T G A A	C G G A C A C G G A	A T A T G C A G G T
551	T T C A C G A C C T	G T T C A A T C C C	A A A C A G G G C G	C G G C T T A C G T	G G T C G T C A A C
601	T T C A T C G C A C	T G T T G G A G C T	T G C C A A A G A A	G G A T T G G T C A	G A A T G T G C A
651	G G A A G A C G G T	T T C G G A G A A A	T C C G A A T C A G	C C T C A A T C A T	G A G G G G G C G C
701	A T T C A G A C G G	C A T T T C C G C	A C A C G A G G C G	G G C G C G A T G T	G T T C T A A

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

m993.pep

1	LKVVLGSFQG	PLDLLLLYLIR	KQNIDVLDIP	MVKITEQYLH	YIAQIETYQF
51	<u>DIAEYLLMA</u>	<u>AMLIEIKSRL</u>	<u>LLPRTEAVED</u>	<u>EEADPRAELV</u>	<u>RRLLAYEQMK</u>
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLGILSRA
151	KHTRSHHEVIK	ETLSVRAQMT	AILRRLNEHG	ICRFHDLFNP	KQGAAYVVN
201	<u>FIALLELAKE</u>	<u>GLVRIVQEDG</u>	<u>FGEIRISLNH</u>	<u>EGAHS</u>	<u>DGIFG</u> TRGRDV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

m993/g993 93.1% identity in 248 aa overlap

m993.pep	10 20 30 40 50 60 LKVVLSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA : : : : : : : : : : : g993 LKVVLGSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQMEAYQFDLAAEYLLMA 10 20 30 40 50 60
m993.pep	70 80 90 100 110 120 AMLIEIKSRLLLPRTEVDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY : : : : : : : : : : : g993 AMLIEIKSRLLLPRTEAVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY 70 80 90 100 110 120
m993.pep	130 140 150 160 170 180 LPLEIAVEAKLPEVYITDLTQAWLGILSRAKHTRSHIVEKETISVRAQMTAILRRLNNGH : : : : : : : : : g993 LPLEIAAAETKLPEVYIADMQAWLGILSRAKHTRSHIVEVIQETLSVRAQMTAILRRLNEHG 130 140 150 160 170 180
m993.pep	190 200 210 220 230 240 ICRFHDLPNPQGAAYVVVNFIALLELAKEGLVRLIVQEDGFGEIRISLNHEGAHSIG : : : : : : g993 ICRFHDLFNPQEQAAYVIVNFIALLELAKEGLVGVQEDGFGEIRISLNHEGAHSIG 190 200 210 220 230 240
m993.pep	249 TRGGRDVF : g993 TRGGRDVF

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

```

1  CTGAAAGTCG TATTGAGCAC TTTCAAGGC CCTTGATC TGCTGCTCTA
51 CCTTATCCGC AAGCAGAACAA TCGATGTTCT CGATATTCCG ATGGTGAAGA
101 TTACCGAACAA GTATCTGCAC TACATGCCAA AAATAGAACAC CTATCAGTT
151 GATTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCTG CTGCTGCCGC GTACCGAACAC CGTCGAAGAC GAAGAACCGC
251 ACCCGCGTGC CGAGTTGGTGC CGCCGCCCTGC TGGCTTAGCA GCAGATGAA
301 CTGGCGGCAC AAGGGTTGGA TGCCTTCCCT CGTGCGGGCC GGGATTTCGC
351 ATGGGCATAC CTGCCACTGG AAAATTGCCGT CGAACGCCAG CTCCCCGAAG
401 TCTATATTAC CGACTTGACG CAGGCCTGGC TGAGTATTT GTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTTATCAA GAAACCATCT CCCTGCGGCC
501 GCAATATGACG GCAATCTGC GCGCTTGGAA CAAACACGGG ATATGCAAGT
551 TTCACGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTGTCACAC
601 TTCAATCGCAC TGTTGGAGCT TGCCAAAGAA GGTTGGTCG GAATCGTACA
651 GGAAGTCGGT TTCCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAAGACGG CATTCCGGC ACACGGGGCG GGCAGCAGTGT GTCTAA

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This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

```

1  LKVVLSSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA
51 DLAAEYLLMA AMLIEIKSRL LLPRTEVDEEADPRAELV RRLLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151 KHTRSHIVEK ETISVRAQM AILRRLNKG ICRFHDLFNP EQGAAYVVVN
201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSIG TRGRDV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

a993.pep	10 20 30 40 50 60 LKVVLSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA : : : : : : m993 LKVVLGSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA
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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLIEIKSRLLLPRTEVDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993	70	80	90	100	110	120
	AMLIEIKSRLLLPRTEVDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAQLSILSRAKHTRSHVIKETISVRAQMTAILRRLNKG					
m993	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAQLGILSPAKHTRSHVIKETISVRAQMTAILRRLNKG					
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPQEKGAAVVVNFIALLAKEGLVGVIVQEVGFGEIRISLNHEGAHSDGSG					
m993	190	200	210	220	230	240
	ICRFHDLFNPKQGAAYVVVNFIALLAKEGLVRIVOEDGFGEIRISLNHEGAHSDGSG					
a993.pep	249					
	TRGGGRDVFX					
m993	249					
	TRGGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGGCGA	GGCGCGTTGC	TTCTTACCGC
51	CTCGGGCAGA	AAATCCGCC	GAACCCACGC	CAAATTCCC	GAAGGAAGCA
101	CCGTGCTTGC	CTTGGGCAT	TCGCTCACCT	TCGGCTACGG	AGCAAACCC
151	GCGGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACGTCGC	GCAAGCCCTA	TCGCGCTGC
251	CCCGCCTGTT	GGCACGCAA	CCCAAGCTTG	TGATTGTCGG	CATAGGGCGC
301	AACGACTTTC	TGCGCAAAGT	TCCCAGGGAG	CAGACCCGGC	CCAATATCGC
351	GAAAATCATC	GAACCCGTGC	AAAAGAAAAA	CATCCCCGCC	GTCCTCGTCG
401	GCGTGC CGCA	CATCACACTG	GGCGCGTTGT	TGCGGCATT	GAGCGACCAT
451	CCGCTGTATG	AGGATTGTC	CGAGGAATAC	GGCATTCCGT	TGTTCGGGCG
501	CCGCTGGCG	GAATTTTGG	GCAATAATAA	TCTGAATTC	GACCAAATCC
551	ACGCCAACCG	CAAAGGCTAT	CGGAAATTG	CCGAAAAATT	GAATCAATT
601	TTGAGAAAAC	ATGGGTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLAGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSAQAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPEE	QTRANIAKII	ETVQKENIPA	VLVGVPHTL	GALFGHLSDH
151	PLYEDLSEYY	GIPLFGGAWA	EILGNNNLKS	DQIHANGKGY	RKFAENLNQF
201	LRKHGFR*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

g996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGGCGA	GGCGCGTTGC	TGCTTACCGC
51	CTCGGGCAGA	AAATCCGCC	GAACCCACGC	CAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCAT	TCGCTCACCT	TCGGCTACGG	CGCAAACCC
151	GCGGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCTGC	CCAAGCCCTG	TCGCGCTGC
251	CCCGCCTGTT	GGCACGCAA	CCCAAGCTTG	TGATTGTCGG	CATAGGGCGC
301	AACGACTTTC	TGCGCAAAGT	TCCCAGGGAG	CAGACCCGGC	CCAATATCGC
351	GAAAATCATC	GAACCCGTGC	AAAAGAAAAA	CATCCCCGCC	GTCCTCGTCG
401	GCGTGC CGCA	CATCACACTG	GGTGC GTTGT	TGCGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTC	CGAGGAATAC	GGCATTCCGT	TGTTCGGGCG
501	CCGCTGGCG	GAATTTTGG	GCGATAATAA	TCTGAATTC	GACCAAATCC
551	ACGCCAACCG	CAAAGGCTAT	CGGAAATTG	CCGAAAGATT	GAATCAATT
601	TTGAGAAAAC	AGGGGTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3010, ORF 996>:

g996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLAGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSAQAL	SRLPALLARK	PKLVIVGIGG

101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKGFR*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10 20 30 40 50 60
	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLAGDSLTFGYGANPGESYPAOLQK
g996	10 20 30 40 50 60
	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLAGDSLTFGYGANPGESYPAOLQK 10 20 30 40 50 60
m996.pep	70 80 90 100 110 120
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
g996	70 80 90 100 110 120
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPPEEQTRANIAKII 70 80 90 100 110 120
m996.pep	130 140 150 160 170 180
	ETVQKENIPAVLVGVPHITL GALFGHLSDH PLYEDLSEEEY GIPLFGGAWAEILGDNNLKS
g996	130 140 150 160 170 180
	ETVQKENIPAVLVGVPHITL GALFGHLSDH PLYEDLSEEEY GIPLFGGAWAEILGDNNLKS 130 140 150 160 170 180
m996.pep	190 200
	DQIHANGKGYRKFAEDLNQFLRKHGFR
g996	190 200
	DQIHANGKGYRKFAENLNQFLRKHGFRX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

```

1 ATGAAACAGAA GAACCTTCCT CCTCGGCAGCA GGCAGCGTTGC TCCTTACCGC
 51 CTGGCGCAGA AAATCCGCCC GAACCCACCG CAAAATTCCC GAAGGAAGCA
101 CGTACTTGC CTTGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
151 GCGGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCCCTCTG
251 CCGCGCTGTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCCGC
301 AACGACTTTC TCGGCAAAGT TCCCAAGGAG CAGACCCGGG CCAATATCGC
351 GAAATCATC GAAACCGGTGCA AGAAGGAAA CATCCCCGCC GTCTCGTCG
401 GCGTGCAGCA CATTACCTTG GGCGCGTTGT TCAGGGCATTG GAGCGATCAT
451 CCGCTGTATG AGGATTGTC CGAGGAATAC GGCATTCCGC TGTTCGCGG
501 CGCGTGGGG GAAATTGTC GCGATAATAA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTG CGGAAGAGTT GAATCAATT
601 TTGAGAAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

```

1 MNRRTFLLGA GALLTACGR KSARTHAKIP EGSTVLAGD SLTFFGYGANP
 51 GESYPAQLQK LTGWNIVNGG VSGDTSQAQL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
201 LRKGFR*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10 20 30 40 50 60
	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLAGDSLTFGYGANPGESYPAQLQK

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
   1 ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
   51 CTGGGCCGCG TTGTCGCCG CCGTCACCTT GGCGCCGCGC GCGCACGTTA
  101 CCCTGTTTG ACGCCGGCG CAGGGGGCG GAAGGGCGG CACACTGGCC
  151 GGAATAATCCG AGCGTTTCGG TTTTTGGAC AAAGGGCAGC ACATTTGGCT
  201 CGGGCATAAC CGGGCGTGT TGCGCCTGAT GAAAACCATC GGTCAGACCC
  251 CCCGTGCGC CTTTTTGCAC GTACCCCTGC ACTGCGCATAT GCACGGCGGT
  301 TTGCACTTGC GCGCCCTCCC CCTGGCCGCG CCGCTGCATA TTTTGGCCG
  351 CGTGTGCTT GCGCCGGCG TACCGCTGC ATTCAAAGCC AAACCTGCTTG
  401 CGCATATGTC CGATTGCAAGTCCGCAC CGCTCGGACAGC CCGCCGACAC
  451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTGC CCGCCGTAAT
  501 GCAGATTGGC CAGCCCCCTGG TCTGGGGCGC GCTAACACAGC CTTTGGAAA
  551 CCGCAAGGCC GCGCGTGTG TGCAAGGTT TGTCCGACGC CGTGTGACG
  601 AAAAATCCG CGACGACTA TCTCTTACCC AAACAGGATT TGGGCCAAT
  651 CGTCGCCGAA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
  701 GCCTCGAAAC GCGCTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTC
  751 CTCGTCACG GCGAAGGCCTT CGATGCCGCATACTTGCCA CCGCGCCCTA
  801 CCACGCCGCG CGCCTCTGC CGAAGGCAC GCGGAACAC GTTCAGACGG
  851 CATATCAAAAC CTCCTCGCTAC CACGCCATCA CCACCGCTCA TCTGCGCTAC
  901 GCCGAACCCG TCCGcCTGcc CGCCCCGCTG ACCGGCATtg CCGAcggcAC
  951 ggcaCaatgG CTGCTTGCc cgGGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAattgc GTTTCCGAcc GCGtccggcG Gtttgaaac
1051 cga

```

This corresponds to the amino acid sequence <SEO ID 3014 ORF 997.ng>.

9997.pep (partial)
1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTIIFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRLIMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPASFAK KLLADMSDLQ KSARLGQPD
151 TWAQWLKQRN VPRAQVMQFW QPLWVGALNT PLETASLRVL CNVLSDGVL
201 KKSGSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPGDKV
251 LVNCEAFDAI ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIAADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 3015>:

```

1 ATGATGAACA CGCGGCATCC GCGCCCCAAA ATCGGGCTCA TCGGGCAGG
51 CTGGGCAGGA CTGTCGCCCG CCGTCACCTT GGCGGGCAC GCGGACGTTA
101 CCCGTGTTGA AGCCGGCCGG CAGGGGGCG GCAGGGCGG CACACTGGCC
151 GGAATACCG AGCGTTTCGG TTTTTGGAC AACGGCAGC ACATTTGGCT
201 CGGGCATACT CGGGGGTGT TGCGCCTGAT GAA-TCATC GGTCGGATC
251 CCCGTGCCG CTTTTGCGC GTACCCCTGC ATGGCATAT CGACGGGGT
301 TTGCAAGTCC GCGCCCTCCC CCTGCCCGC CCGCTGCATA TTTTGGGGG
351 CGTGTGCTT GCGGGCGGTG CACCGACTGC ATTCAAAGCC AAACGTGTTG
401 CGGATATGTC CGATTGCG AAGTCGGCAG GCCTCCGAA GCCGGCACAGC
451 CAAGTGGCCG AATGGTGAAG CAGGGGAAC GTGCCGGCTG CGGGCGTGT
501 GCAGTTTGG CAGGGCTGTTTGGGGCGC GCTCAACAGC CCTTGGGAA

```

551	CCCGAACGCT	GCGCGTGTG	TGCAAATT	TGTCGGACGG	CCTGCTGACGG
601	AAAAATTCGG	GCAGCGACTA	TCTCCTACCC	AAGCAGGATT	TGGGCGCAAT
651	CGTCGCCGAA	CCCGCCTTGG	CGGATCTCA	ACGGCTCGGG	GGGGACATCC
701	GCCCTGAACG	GCGCGTATGC	CTCTGAAACA	CCCTCCGGGA	GGGGAAATGG
751	CTCGTCAACG	GCGAAGCTTT	CGATGCCGCC	GTCGGCGCCA	CCGGCGCCCTA
801	CCACGCCGCC	GCGCTCTGC	CCGAAGGCAC	GCCCCAACAC	GTTACAGACGG
851	CATATCAAAA	CTTCTGTAC	CACCGCCATCA	CCACCGCTCA	TCTGCGCTAC
901	GCGGAAACCCG	TCCGGCTCGG	GGGGCCCGCTG	ACGGGUTTG	CCGACGGCAC
951	GGTGCAATGG	CTGCTTGC	GGGGCAGGCT	CGGACTGCCT	AAAAACGAAG
1001	TGTGCGCCGT	CATCAGCGTT	TCCGACCCGG	TGGCGCCGT	TGCAAACCGG
1051	GCGTGGGGCG	AAAGAGCCCA	GGCGGACACTC	AAACAGCATC	TTCGGCGATC
1101	GGGGGAACCCG	GAAGCGCTG	GGCGTATCAC	CGAAAAGACCG	GGCACAAACCG
1151	CAGCGGATGC	CCCGCCGCCG	GAACGGTGTG	GGTTGCACCG	GCACCGCATC
1201	TTCCCCGCCG	GGCAACTACCT	CCACCCGGAC	TACCCCGCCA	CGCTCGAAAGC
1251	CGCCGTACA	TCAGGTTCG	CGTCGGCGGA	AGCCTGCCTG	CAAAGCGTGA
1301	GGCATGCCGT	CTGA			

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>;

m997.pep

```

 1 MMONPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEEAGR QAGGRARTLA
 51 GNTDGFGLD NGQHILLGAY RGVLRLMLKTI GSDPRAAFLR VPLWHMHGG
101 LOFRALPLPA PHILGGVLL ARRATPAFKA KLLADMSDLQ KSARLGQDPT
151 TVAOWLQORN PVRAAVMQFW QPLVWGAINT PLETASLRL CNVLSGDVLT
201 KKSGSDYLLP KQDLGAIVAE PALADLQRGL ADIRLETRVC RLNTLPDKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPPL TGLADGTVQW LLCRGRGLGP ENEVASIVIS SDRVGAFAFN
351 AWADKAHADL KRILPHLGEV EAERVITEKR ATTAADAPP DLSWLHRHRI
401 FPGADYLHPD YPATLEAAAVO SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*.

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD					
m997						
	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g997.pep	NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997						
	NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQOWLQQRNVPRAAVMQFWQPLVWGALNT					
m997	:	:	:	:	:	:
	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQOWLQQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g997.pep	PLETASLRVLCNVLSDGVLTKSGSDYLLPKODLGAIAEPAELQRLGADIRLETRVC					
m997						
	PLETASLRVLCNVLSDGVLTKSGSDYLLPKODLGAIAEPAELQRLGADIRLETRVC					
	190	200	210	220	230	240
	250	260	270	280	290	300
g997.pep	RLNTLPDGKVVLNGEAFDAIILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
m997	:	:	:	:	:	:
	RLNTLPDGKVVLNGEAFDAIILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
	310	320	330	340	350	
g997.pep	AEPVRLPAPLTGIADGTAQWLCPGQPQDCPQNEVSAVISVSDRVGAFANR					
m997	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :
	AEPVRLPAPLTGLADGTVQWLRCRGL-GLPENEVSAVISVSDRVGAFANRAWADKAHD					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

a997.seq

```

1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCCGAGG
51  CTGGGCCGGC TTGTCCGCCG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTGA AGCCCGGCCGG CAGCCGGGGC GCAGGGCGGG CGCACTGGCC
151 GGAATAACCG ACGGTTTCGG TTTTTGGAC AACGGGCAGC ATATTTACT
201 CGGCCCATAC CGGGGGCGTGT TGCGCCTGAT GAAACACATC GGTTCAGACC
251 CCCATGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAAGTTC CGCGCCTCCC CCTGCCCGGG CCCCTGCATA TTTTGGCGGG
351 CGTGTGCTT TACCGTCCGC ATTCAAAGCC AAACGTCTTG
401 CGGATATGTC CGATTGCGAG AAGTCGCAAC GCGTCGGACA GCCCGACAGG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGCTAAT
501 GCAGTTTGG CAGCCCTTGG TTGGGGCGC GCTAACACGG CCTTTGGAAA
551 CGCGAACGCG CGCGCCTTGC TGCAACAGTT TGTCGGACGG CGTGCTGACG
601 AAAATAACCG GCAGCGACTA TCTCTTACCC AAACAGGATT TGGGGCAAT
651 CGTCGCCGA CCGCCTTGG CGGAGCTTCA ACGGCTCGGC CGGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCTCCCCGGA CGGGAAAGTG
751 CTCGTCAACCG GCGAACCTTT CGATGCCGC GTCGCCGCAC CGCGCCCTA
801 CGACGCCGC GCGCTCCTGC CGAAGGCAAC GCGCAACAC GTTCAGACGG
851 CATATCAAA CCTCGCTAT CACGCCATCA CCACCGCTTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCCGCTG ACCGGACTTG CCGACGGCAC
951 GGTCGAATGCG CTGCTTTGCC GGGGAGGCGT CGGACTGCCT GAAARCGAAG
1001 TGTCGGCCGT CATACCGCTT TCCGACCGGC TCAGCCGTT TGCAAACCGG
1051 CGCTGGCGC ACAAGGTTCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACCG GCCACAACCG
1151 CAGCCGATGC CCGCCGGCCG GATTGTCGT GTTGCACCG CGACCGCATC
1201 TTCCCGTACCA TCAGGTTTCG CGTCGGCGGA AGCTGCCCTG CAAAGCTGA
1251 CGCGGTACAA TGATGCCGT CTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

a997.pep

```

1  MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRALA
51  GNTDGFGLD NGQHILLGAY RGVLRLMKTI GSDPHAAFLR VPLWHMHCG
101 LQFRALPLPA PLHILGGVLL ARRVPASAFKA KLLADMSDLQ KSARLGQPDT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGAINT PLETASLRVL CNVLSDGVL
201 KKSGSDYLLPK QDILGAIVAE PALAEQLRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLEPGTPEH VOTAYQNLY HAITTVYI
301 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFA
351 AWADKVKHADL KRILPHLGEV EAERVITEKR ATTAADAPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

a997.pep	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRALA	LAGNTDGFGFLD
m997	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTL	AGNTDGFGFLD
a997.pep	10 20 30 40 50 60	
	NGQHILLGAYRGVLRLMKTI	GSDFHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL
m997	10 20 30 40 50 60	
	NGQHILLGAYRGVLRLMKTI	GSDFPRAAFLRLPVLWHMHGGLQFRALPLPAPLHILGGVLL
	70 80 90 100 110 120	
a997.pep	130 140 150 160 170 180	
	ARRVPSAFKAKLLADMSDLQKSARLGQPDFTVAQWLQQRNVPR	AAMQFWQPLVWGALNT
m997	130 140 150 160 170 180	
	ARRAPTAFKAKLLADMSDLQKSARLGQPDFTVAQWLQQRNVPR	AAMQFWQPLVWGALNT
	190 200 210 220 230 240	
a997.pep	PLETASLRVLNVLSDGVLTKSGSDYLLPKQDLGAIVAEPALAEQLRLGADIRLETRIC	

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m997	PLETASLRVLCNVLSDGVLTKSGSDYLLPKQDLGAIVAEPALADLQLRGADIRLETRVC					
	190	200	210	220	230	240
	250	260	270	280	290	300
a997.pep	RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTEPEHVQTAYQNLRYHAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTEPEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
	310	320	330	340	350	360
a997.pep	AEPVRLPAPLTGLADGTQWLLCRGRGLPENEVSAVISVSDRVGAFAFANRAWADKVHADL					
m997	AEPVRLPAPLTGLADGTQWLLCRGRGLPENEVSAVISVSDRVGAFAFANRAWADKAHADL					
	310	320	330	340	350	360
	370	380	390	400	410	420
a997.pep	KRILPHLGEPEAVRVITEKRATTAADAPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ					
m997	KRILPHLGEPEAVRVITEKRATTAADAPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ					
	370	380	390	400	410	420
	430					
a997.pep	SGFASAEACLQSLSDAVX					
m997	SGFASAEACLQSLSDAVX					
	430					

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

m999.seq	1 ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC					
	51 AGCCTGCAAC CAAACAATCAA AAAC					
	101 GTATCCAGGC TGCTGATTGT ACCGGCCCAA TGGACATCAC AGTGACAA					
	151 TATCTCATCA ATTGGAGCA AGCATTAAACTCAGAACG TCTCAACAAA					
	201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT					
	251 TGGTAATGGA TTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA					
	301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG					
	351 ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAAGGAG					
	401 TTCTGTCCTT AACTACCACA GACAAATTGG GCGGAATCCGA AGCAGGAAAA					
	451 CAACTTTTA CAGCTTTAAC CGAACGTCGTC AAAGAAATCCA ATCAGACAGG					
	501 AGCAACAGCG CAAAAAGACG TTCCGGCAGA TGGTATTAA TATAGCGTTG					
	551 TTTTGAAAA AGAAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAAACCC					
	601 TAA					

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

m999.pep	1 MNMKKLISAI CVSIVLSCACN QQSFTAQAEV PVQSIQAADC TAPMDITVEQ					
	51 YLINLEQAFK TQNVSTKIHN KNIVKTDGCV DLTLMDFGA IALKLDEQQK					
	101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTTE DKLGESEAGK					
	151 QLFTALTEVV KESNQTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP					

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

1420

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

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16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

09/674546

WO 99/57280

1/30

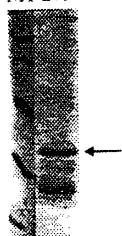
PCT/US99/09346

279 (10.5 kDa)

Fig. 2

A) PURIFICATION

M1 279

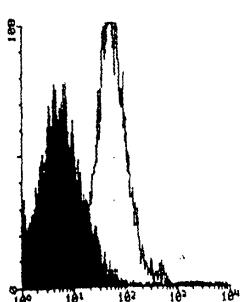


B) WESTERN BLOTH

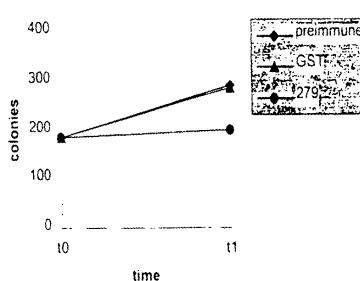
TP OMV



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract, OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B)

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576 (27.8 kDa)

Fig. 3

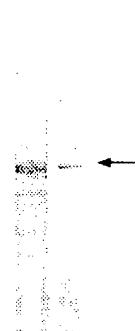
A) PURIFICATION

M1 576



B) WESTERN BLOTH

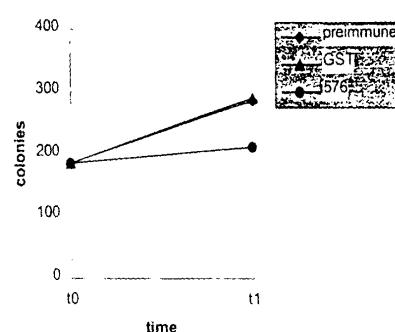
TP OMV



C) FACS



D) BACTERICIDAL ASSAY



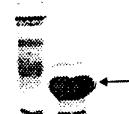
E) ELISA assay: positive

576

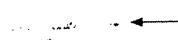
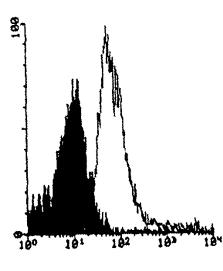
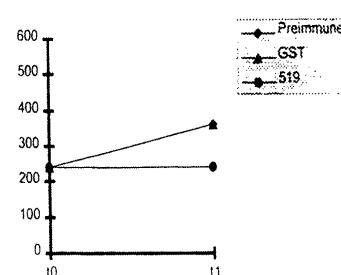
The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

519 (33 kDa)**A) PURIFICATION**

M1 519

**B) WESTERN BLOTH**

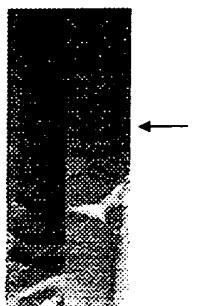
TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

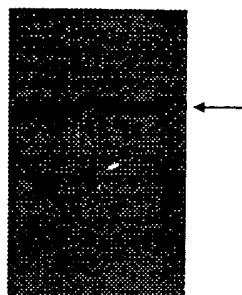
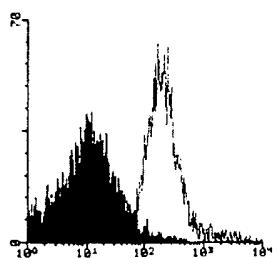
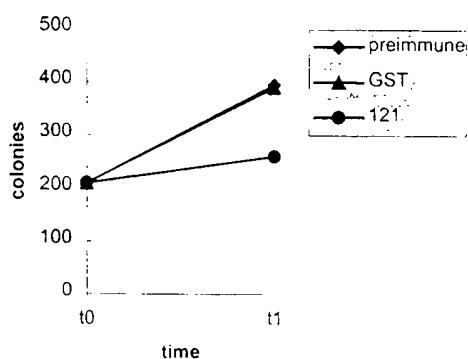
The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

**B) WESTERN BLOTH**

TP OMV

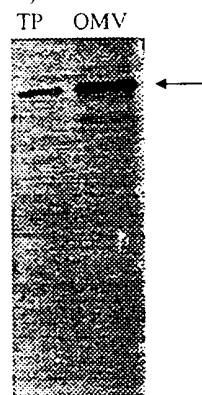
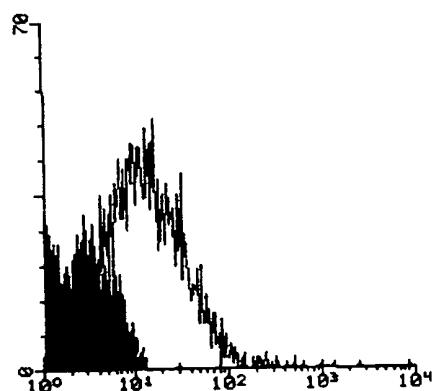
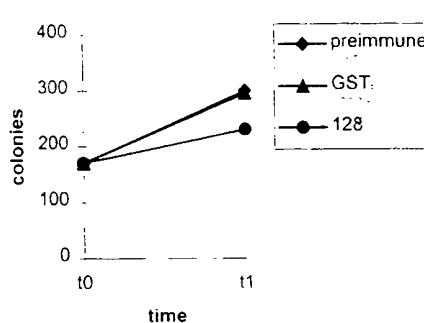
**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 5

128 (101 kDa)

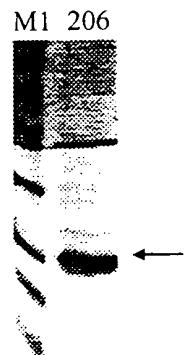
Fig. 6

A) PURIFICATION**B) WESTERN BLOTH****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

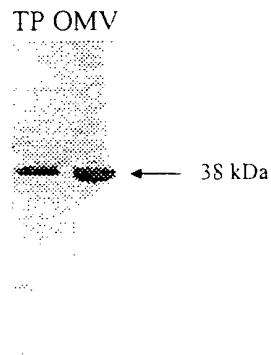
The predicted gene 128 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

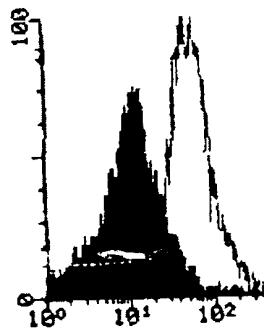
A) PURIFICATION



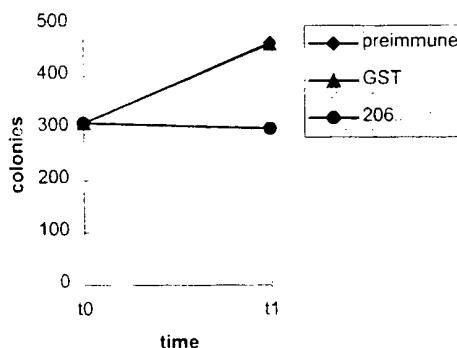
B) WESTERN BLOTH



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

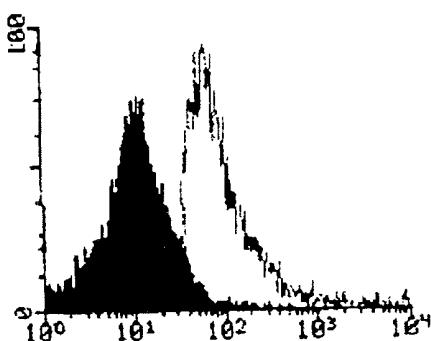
287 (78 kDa)

Fig. 8

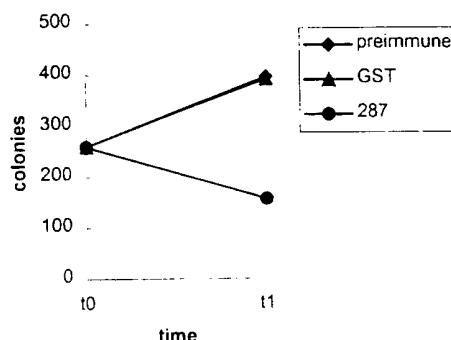
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

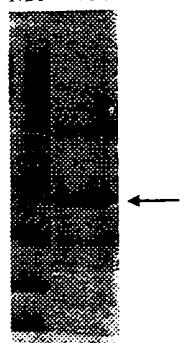
D) ELISA assay : positive

287

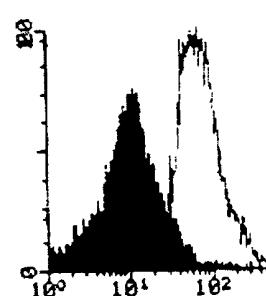
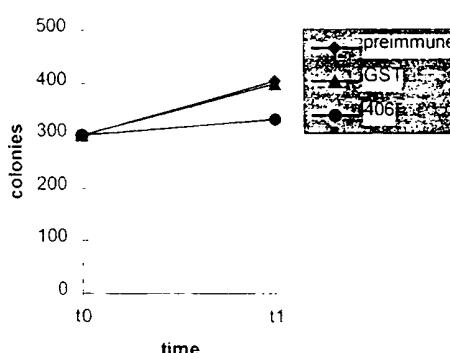
The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

406 (33 kDa)**Fig. 9****A) PURIFICATION**

M1 406

**B) WESTERN BLOTH**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay : positive****406**

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

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Hydrophilicity Plot, Antigenic Index and AMPHI Regions

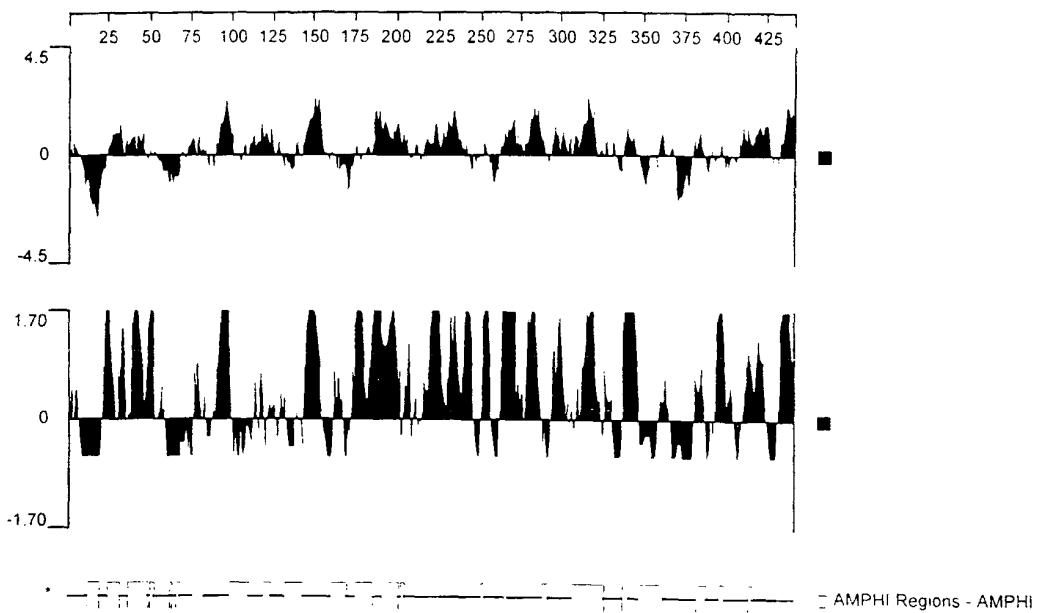


Fig. 10

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Hydrophilicity Plot, Antigenic Index and AMPHI Regions

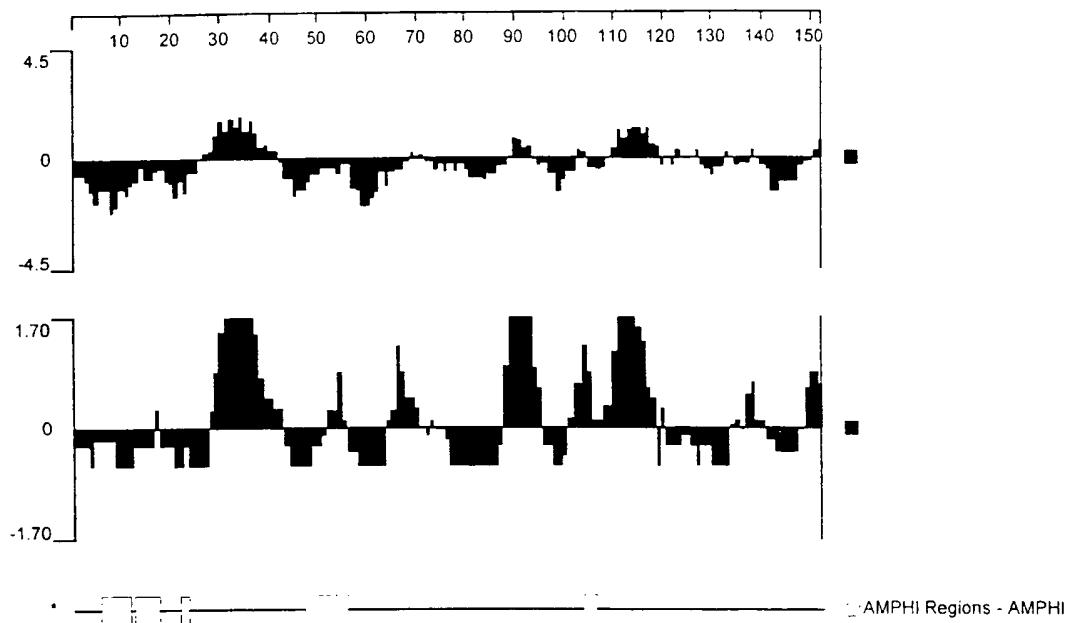


Fig. 11

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576-1

Hydrophilicity Plot, Antigenic Index and AMPHI Regions

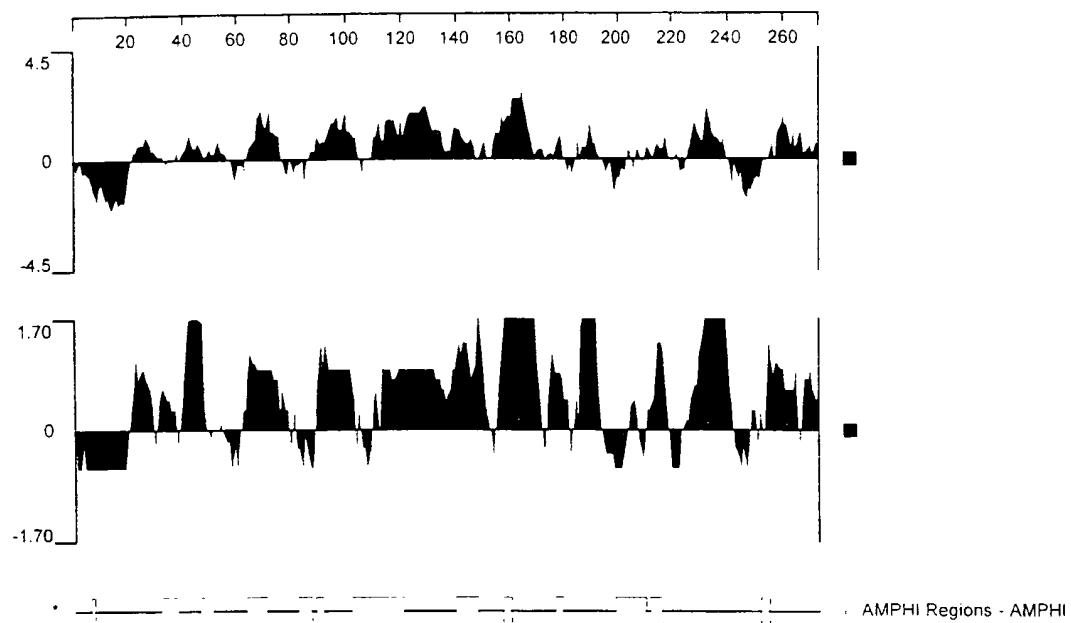


Fig. 12

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519-1

Hydrophilicity Plot, Antigenic Index and AMPHI Regions

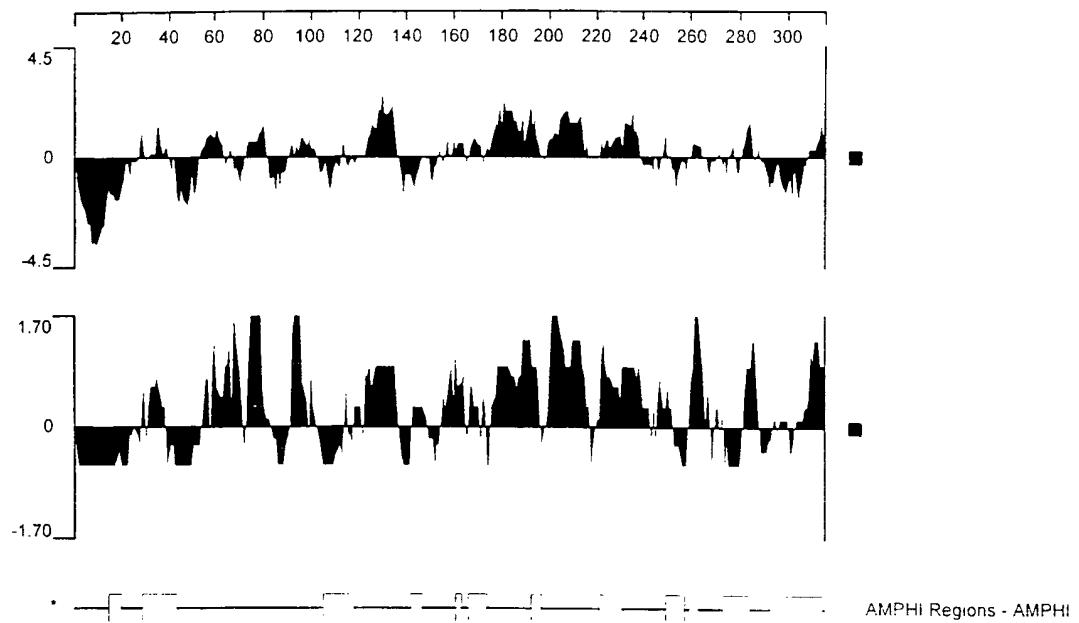


Fig. 13

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Hydrophilicity Plot, Antigenic Index and AMPHI Regions

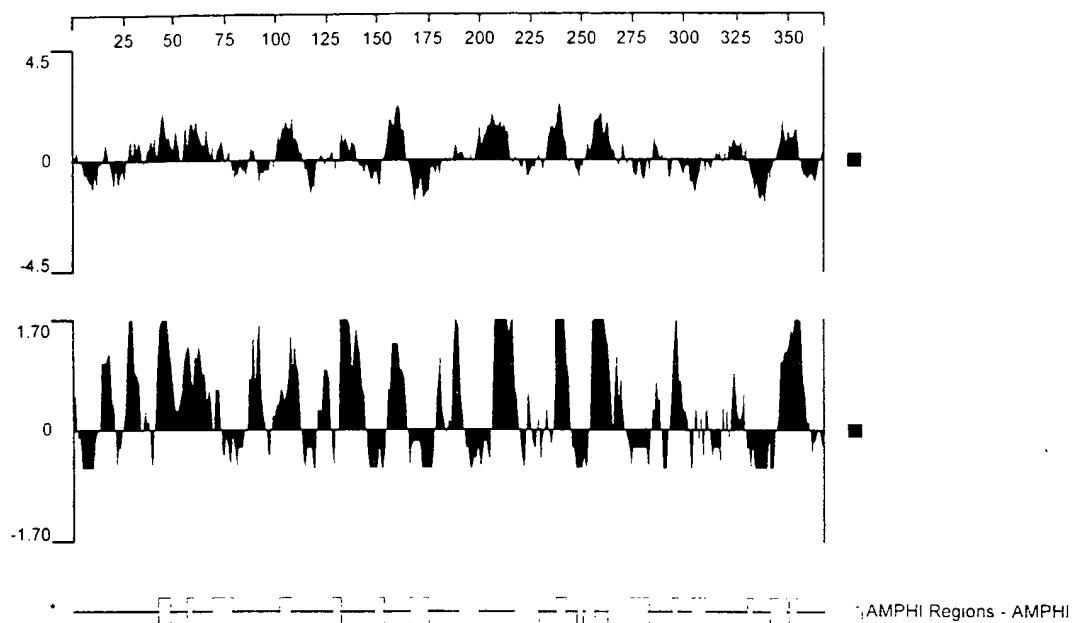


Fig. 14

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128-1

Hydrophilicity Plot, Antigenic Index and AMPHI Regions

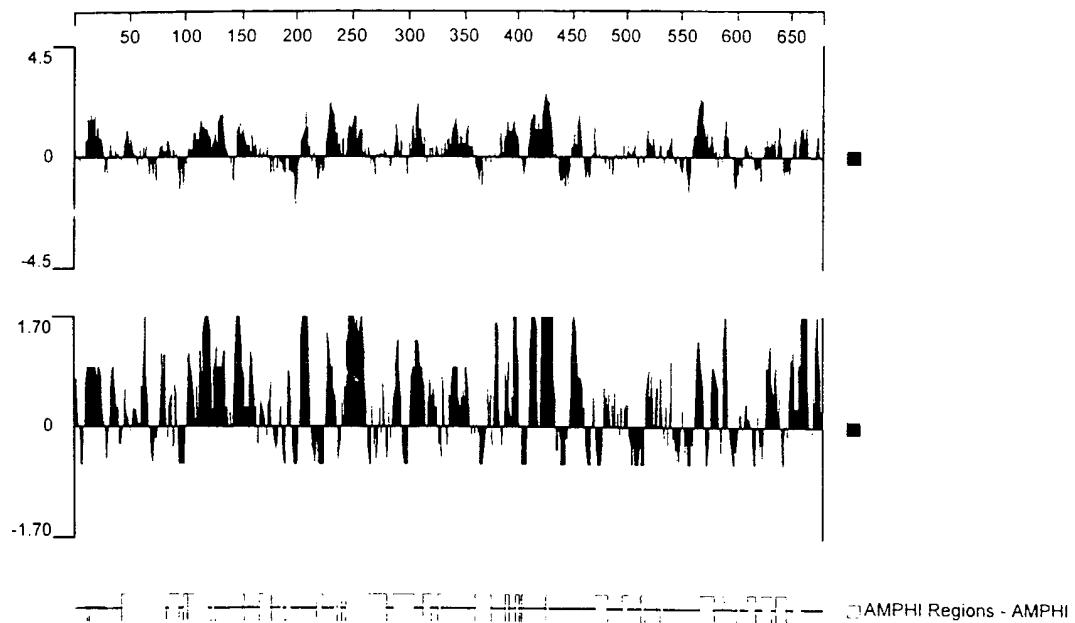


Fig. 15

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Hydrophilicity Plot, Antigenic Index and AMPHI Regions

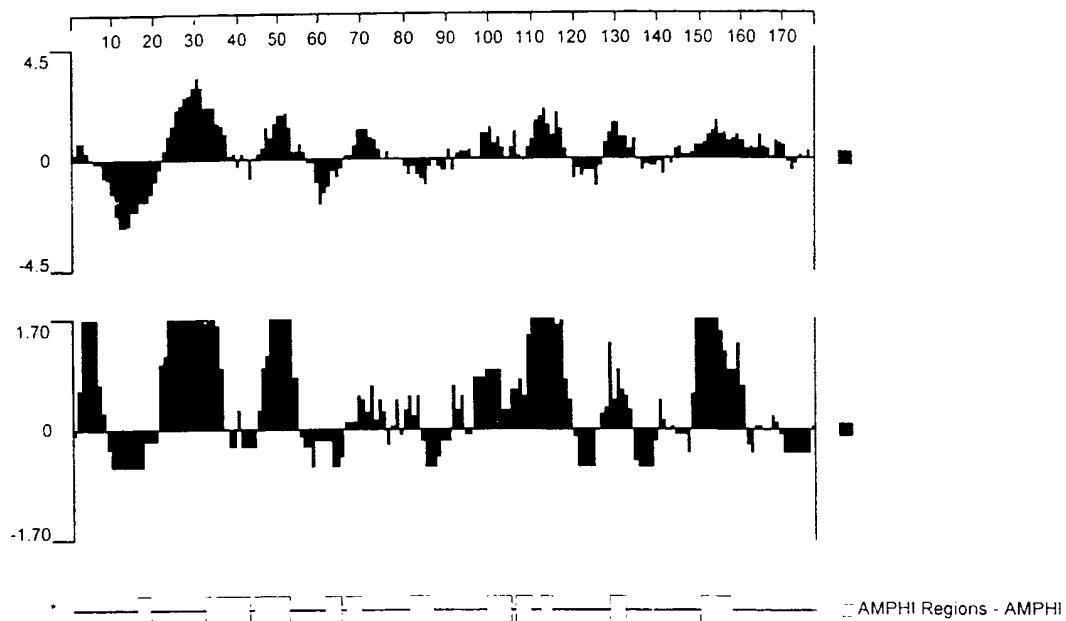


Fig. 16

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Hydrophilicity Plot, Antigenic Index and AMPHI Regions

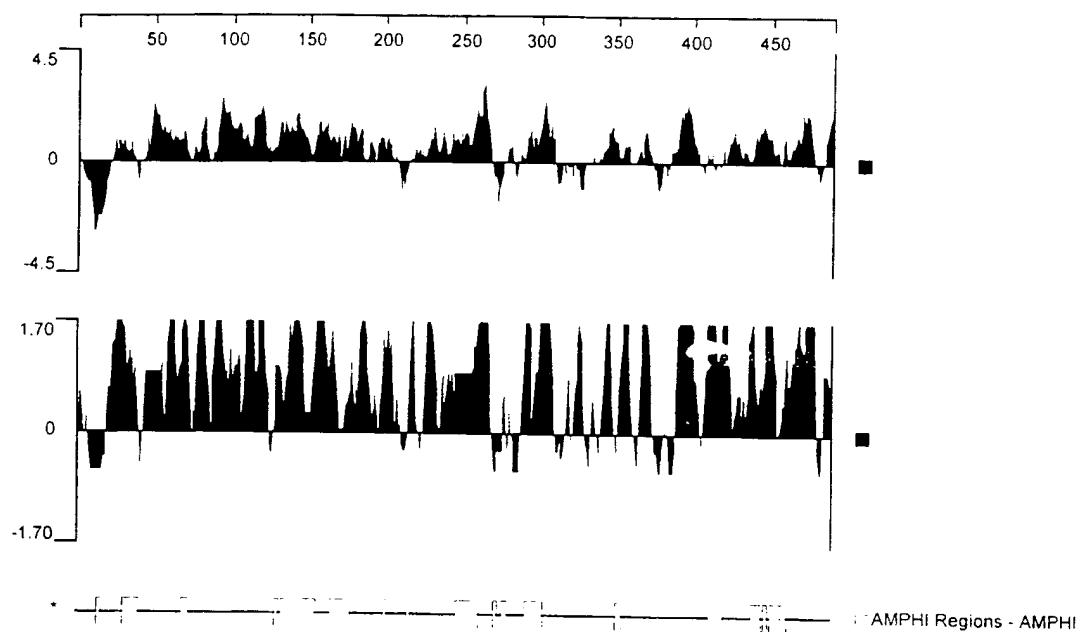


Fig. 17

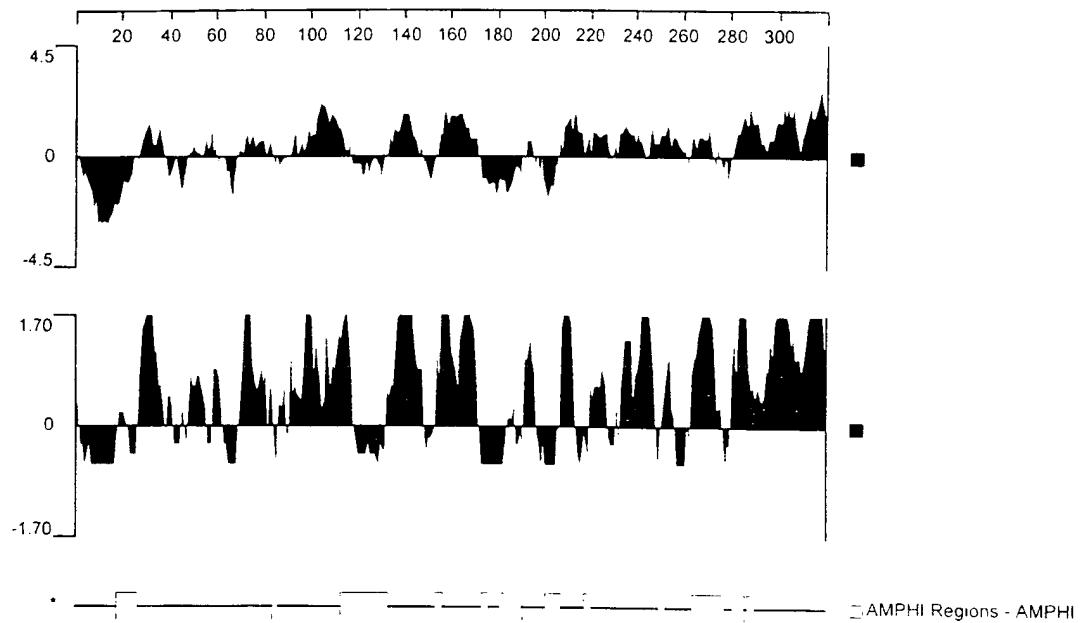
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

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z05_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z08_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z2491 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z11_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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z01_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z09_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z12_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z22_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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z26_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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fa1090 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z32_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z33_225 1 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG

z05_225 61 NADELIGSAMGLNE.....
z08_225 61 NADELIGSAMGLNE.....
z2491 61 NADELIGSAMGLNEQPVLVPNRVPARRAGNADELIGNAMGLNEQPVLVPNRVPARRAGNA
z11_225 61 NADELIGSAMGLNEQPVLVPNRVPARRAGNADELIGNAMGLNEQPVLVPNRVPARRAGNA
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z09_225 61 NADELIGSAMGLNE.....
z12_225 61 NADELIGSAMGLNE.....
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z24_225 61 NADELIGSAMGLNF.....
z25_225 61 NADELIGSAMGLNE.....
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z13_225 61 NADELIGSAMGLNE.....
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z15_225 61 NADELIGSAMGLNE.....
fa1090 61 NADELIGSAMGLNE.....
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z33_225 61 NADELIGSAMGLNE.....

Fig. 19A

Fig. 19B

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zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

Fig. 20A

gnmzq09	121	YQILDSVTTVSAAJARLVDSRNGKVWWSGSASIREGSNNNSGGLGALVSAVVNQIANSLT
gnmzq31	121	YQILDSVTTVSAAJARLVDSRNGKVWWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
fa1090	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq32	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq33	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq01	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq05	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq08	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq02	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq03	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq04	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq07	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq10	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq11	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq13	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq15	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq16	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq17	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq19	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq21	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq22	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq23	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq24	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq25	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq27	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq28	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq29	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
z2491	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq14	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq18	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq26	121	YQILDSVTTVSAAKARLVDSRNGKEWLWSGSASIREGSNNNSGGLGALVCAVVNQIANSLT
gnmzq09	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq31	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
fa1090	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq32	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq33	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq01	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq05	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq08	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq02	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq03	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq04	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq07	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq10	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq11	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq13	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq15	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq16	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq17	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq19	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq21	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq22	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq23	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq24	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq25	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq27	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq28	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq29	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
z2491	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq14	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq18	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq26	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Fig. 20B

287_14	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
287_2	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
287_21	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
z2491	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
287_9	1	MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
fa1090	1	MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVSE	KETEA
287_14	50	KEDAPOQGSQGQGAPSQOGQDMAAVSEENTNGGAAATDKPKNEDEGAQNDMPQNAADT	
287_2	50	KEDAPOQGSQGQGAPSQOGQDMAAVSEENTNGGAAATDKPKNEDEGAQNDMPQNAADT	
287_21	50	KEDAPOQGSQGQGAPSQOGQDMAAVSEENTNGGAAATDKPKNEDEGAQNDMPQNAADT	
z2491	50	KEDAPOQGSQGQGAPSQOGQDMAAVSEENTNGGAAATDKPKNEDEGAQNDMPQNAADT	
287_9	61	VSGAPQADTODATAGKGGDMAAVSAENTNGGAAATTDPNPKNEDEGAQNDMPQNAADT	
fa1090	61	AGGAQADTODATAGKGSQDMAAVSAENTNGGAAATTDPNPKNEDEGAQNDMPQNAADT	
287_14	110	DSSLTPNHTPASNMPPAGNMEHQADAGESEQPANQPDMANADGMQGDDPSAGGENAGNTA	
287_2	110	DSSLTPNHTPASNMPPAGNMEHQADAGESEQPANQPDMANADGMQGDDPSAGGENAGNTA	
287_21	110	DSSSTPNHTPDPNMLAGNMEHQADAGESQPANQPDMANADGMQGDDPSAGGENAGNTA	
z2491	110	DSSSTPNHTPDPNMLAGNMEHQADAGESQPANQPDMANADGMQGDDPSAGGENAGNTA	
287_9	119	DSSSTPNHTPAPNMPTRDNGNQADAGESAQPANQPDMANADGMQGDDPSAGGENAGNTA	
fa1090	117	
287_14	170	AQETNQAEENNQTAGSQNPASSNTNPSSATNSCGDFGRTNVCNSV	IDGPSQNITLTHCKGDS
287_2	170	AQETNQAEENNQTAGSQNPASSNTNPSSATNSCGDFGRTNVCNSV	IDGPSQNITLTHCKGDS
287_21	170	AQETNQAGNNQAGSSDPIPASNPAPANGCSNFGRVDLNGV	IDGPSQNITLTHCKGDS
z2491	170	AQETNQAGNNQAGSSDPIPASNPAPANGCSNFGRVDLNGV	IDGPSQNITLTHCKGDS
287_9	178	DQIANQAEENNQVEGSQNPASSNTNPATNGSDFGRINVANGEREDSGSNYTLTHCKDVK	
fa1090	117	ESANQGTGNQNPAGSSDSDAPASNPAPANGCSDFGRTNVCNSV	IDGPSQNITLTHCKGDS
287_14	230	CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNKFKVGLVADSQVMKGINNOXII	
287_2	230	CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNKFKVGLVADSQVMKGINNOXII	
287_21	230	CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNKFKVGLVADSQVMKGINNOXII	
z2491	230	CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNKFKVGLVADSQVMKGINNOXII	
287_9	238	CDRD.FLDEEAPPKSEFEKLSDAKINKYKKDEQRNFVGLVADRVEKNGTNKYII	
fa1090	176	CNGDNLLDEEAPS KSEFEKLSDAKINKYKKDEQRNFVGLVADRVKKDGTNKYII	
287_14	290	FYKPKP.TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG	
287_2	290	FYKPKP.TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG	
287_21	286	FYKPKP.TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG	
z2491	286	FYKPKP.TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG	
287_9	293	IYKDKSASSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG	
fa1090	232	FYTDKPKT.....RSARSRRLSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG	
287_14	348	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGNAVYNGEVLFH	ENGRPSPLGRFAA
287_2	348	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGNAVYNGEVLFH	ENGRPSPLGRFAA
287_21	344	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGNAVYNGEVLFH	ENGRPSPLGRFAA
z2491	344	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGNAVYNGEVLFH	ENGRPSPLGRFAA
287_9	353	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGNAVYNGEVLFH	ENGRPSPLGRFAA
fa1090	285	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGNAVYNGEVLFH	ENGRPSPLGRFAA
287_14	408	KVDFGSKSVDGIIDSGDGLHMGTQKFKAIDGNGFKGTWTENGCGDVSG	FYGPAGEEEVA
287_2	408	KVDFGSKSVDGIIDSGDGLHMGTQKFKAIDGNGFKGTWTENGCGDVSG	FYGPAGEEEVA
287_21	404	KVDFGSKSVDGIIDSGDGLHMGTQKFKAIDGNGFKGTWTENGCGDVSG	FYGPAGEEEVA
z2491	404	KVDFGSKSVDGIIDSGDGLHMGTQKFKAIDGNGFKGTWTENGCGDVSG	FYGPAGEEEVA
287_9	413	KVDFGSKSVDGIIDSGDGLHMGTQKFKAIDGNGFKGTWTENGCGDVSG	FYGPAGEEEVA
fa1090	345	KVDFGSKSVDGIIDSGDGLHMGTQKFKAIDGNGFKGTWTENGCGDVSG	FYGPAGEEEVA

FIG. 21A

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287_14	468	GKYSYRPTDAEKGGFGVFA GKKEQD
287_2	468	GKYSYRPTDAEKGGFGVFA GKKEQD
287_21	464	GKYSYRPTDAEKGGFGVFA GKKEQD
z2491	464	GKYSYRPTDAEKGGFGVFA GKKEQD
287_9	473	GKYSYRPTDAEKGGFGVFA GKKEQD
fa1090	405	GKYSYRPTDAEKGGFGVFA GKKEQD

FIG. 21B

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z2491_519	1	MEFFIILLAAVVFVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv26_519	1	MEFFIILLAAVVFVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv22_519ass	1	MEFFIILLAAVVFVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
fa1090_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv32_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv11_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv28_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv96_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv02_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv03_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv04_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv05_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv01_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv07_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv12_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv18_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv19_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv21_519ass	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv27_519	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv20_519ass	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv06_519ass	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv29_519ass	1	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRLTAGLNILIPFIDRVAYRHSL

z2491_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv26_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv22_519ass	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
fa1090_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv32_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv11_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv28_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv96_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv02_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv03_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv04_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv05_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv01_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv07_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv12_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv18_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv19_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv21_519ass	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv27_519	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv20_519ass	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv06_519ass	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG
zv29_519ass	61	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSNNYIMAITQLAQTTLRSVIG

z2491_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519ass	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass	121	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

FIG. 22A

z2491_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

z2491_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv26_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv22_519ass	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
fa1090_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv32_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv11_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv28_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv96_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv02_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv03_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv04_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv05_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv01_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv07_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv12_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv18_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv19_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv21_519ass	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv27_519	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv20_519ass	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv06_519ass	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL
zv29_519ass	241	LVAEANAEAIRQIAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPAVADIGSL

z2491_519	301	ISAGMKIIDSSKTAK*
zv26_519	301	ISAGMKIIDSSKTAK*
zv22_519ass	301	ISAGMKIIDSSKTAK*
fa1090_519	301	ISAGMKIIDSSKTAK*
zv32_519	301	ISAGMKIIDSSKTAK*
zv11_519	301	ISAGMKIIDSSKTAK*
zv28_519	301	ISAGMKIIDSSKTAK*
zv96_519	301	ISAGMKIIDSSKTAK*
zv02_519	301	ISAGMKIIDSSKTAK*
zv03_519	301	ISAGMKIIDSSKTAK*
zv04_519	301	ISAGMKIIDSSKTAK*
zv05_519	301	ISAGMKIIDSSKTAK*
zv01_519	301	ISAGMKIIDSSKTAK*
zv07_519	301	ISAGMKIIDSSKTAK*
zv12_519	301	ISAGMKIIDSSKTAK*
zv18_519	301	ISAGMKIIDSSKTAK*
zv19_519	301	ISAGMKIIDSSKTAK*
zv21_519ass	301	ISAGMKIIDSSKTAK*
zv27_519	301	ISAGMKIIDSSKTAK*
zv20_519ass	301	ISAGMKIIDSSKTAK*
zv06_519ass	301	ISAGMKIIDSSKTAK*
zv29_519ass	301	ISAGMKIIDSSKTAK*

Fig. 22B

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Fig. 23A

fa1090	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRTERARFPPIYGIPDDFISVPLPAGLRLRGKNA z...3asbc
zm32asbc	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRTERARFPPIYGIPDDFISVPLPAGLRLRGKNA zm23asbc
zm27bc	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm09
zm10	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm24
zm25	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm14
zm04	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm11asbc
zm08n	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm96
zm01	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm02
zm03	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm07
zm12	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm18
zm19	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm20
zm21	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm06
zm17	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm13
zm05	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA z2491
zm22	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm26
zm28	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm29asbc
zm16	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA zm15
zm31asbc	121	YFTPWQVAGNGSLAGTVTGYEPVLKGDRRRTAQARFPPIYGIPDDFISVPLPAGLRLRGKNA fa1090
zm33asbc	181	LVRIRQTGKNSGTIDNAGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm32asbc
zm23asbc	181	LVRIRQTGKNSGTIDNAGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm27bc
zm09	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm10
zm24	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm25
zm14	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm04
zm11asbc	181	LVRIRQTGKNSGTIDNAGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm08n
zm96	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm01
zm02	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm03
zm07	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm12
zm18	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm19
zm20	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm21
zm06	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm17
zm13	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm05
z2491	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm22
zm26	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm28
zm29asbc	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm16
zm15	181	LVRIRQTGKNSGTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm31asbc
	181	LVRIRQTGKNSGTIDNAGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL

Fig. 23B

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Fig. 23C

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fa1090	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm33asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm32asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm09	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm10	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm24	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm25	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm14	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm04	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm96	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm01	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm02	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm03	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm07	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm12	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm18	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm19	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm20	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm21	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm06	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm17	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm13	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm05	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
z2491	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm22	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm26	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm28	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm16	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm15	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMMPKEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm27bc	421	MKEPGYVWQILPNGMMPKEYRP*
zm09	421	QKTTGYVWQLLPNGMMPKEYRP*
zm10	421	QKTTGYVWQLLPNGMMPKEYRP*
zm24	421	QKTTGYVWQLLPNGMMPKEYRP*
zm25	421	QKTTGYVWQLLPNGMMPKEYRP*
zm14	421	QKTTGYVWQLLPNGMMPKEYRP*
zm04	421	QKTTGYVWQLLPNGMMPKEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm08n	421	QKTTGYVWQLLPNGMMPKEYRP*
zm96	421	QKTTGYVWQLLPNGMMPKEYRP*
zm01	421	QKTTGYVWQLLPNGMMPKEYRP*
zm02	421	QKTTGYVWQLLPNGMMPKEYRP*
zm03	421	QKTTGYVWQLLPNGMMPKEYRP*
zm07	421	QKTTGYVWQLLPNGMMPKEYRP*
zm12	421	QKTTGYVWQLLPNGMMPKEYRP*
zm18	421	QKTTGYVWQLLPNGMMPKEYRP*
zm19	421	QKTTGYVWQLLPNGMMPKEYRP*
zm20	421	QKTTGYVWQLLPNGMMPKEYRP*
zm21	421	QKTTGYVWQLLPNGMMPKEYRP*
zm06	421	QKTTGYVWQLLPNGMMPKEYRP*
zm17	421	QKTTGYVWQLLPNGMMPKEYRP*
zm13	421	QKTTGYVWQLLPNGMMPKEYRP*
zm05	421	QKTTGYVWQLLPNGMMPKEYRP*
z2491	421	QKTTGYVWQLLPNGMMPKEYRP*
zm22	421	QKTTGYVWQLLPNGMMPKEYRP*
zm26	421	QKTTGYVWQLLPNGMMPKEYRP*
zm28	421	QKTTGYVWQLLPNGMMPKEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm16	421	QKTTGYVWQLLPNGMMPKEYRP*
zm15	421	QKTTGYVWQLLPNGMMPKEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMMPKEYRP*

Fig. 23D